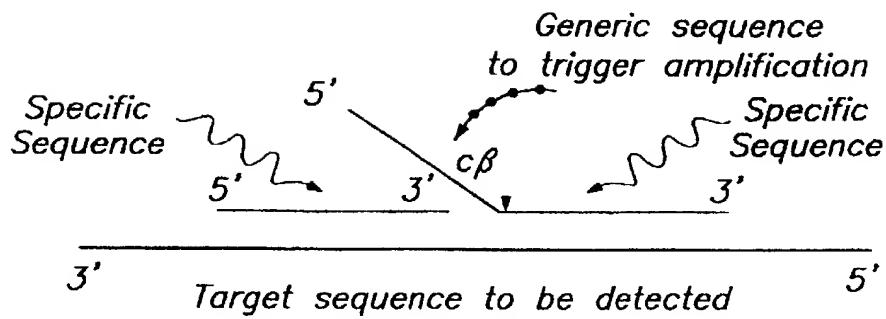
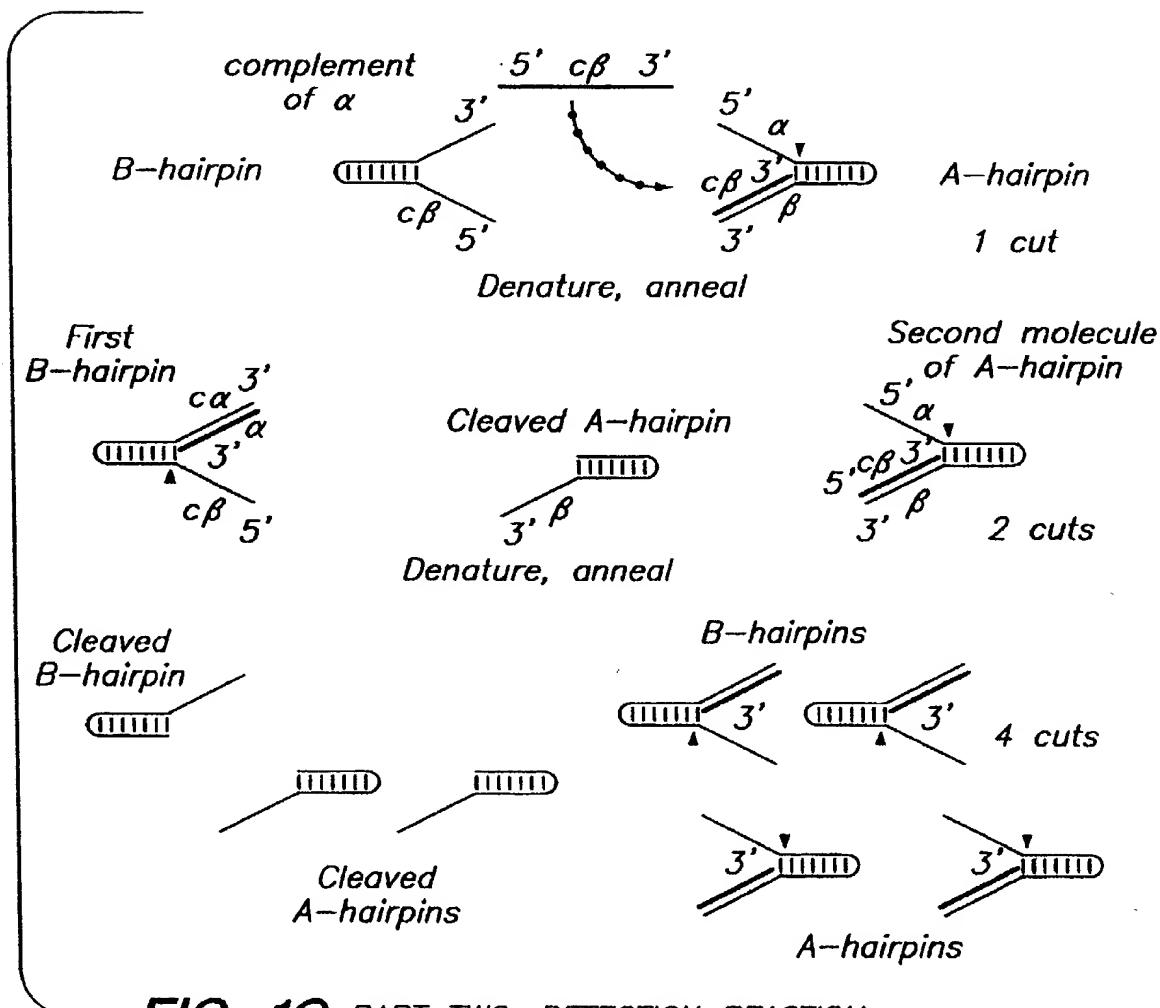


**FIG. 1A**



**FIG. 1B PART ONE: TRIGGER REACTION**



**FIG. 1C PART TWO: DETECTION REACTION**

FIG. 2A

MAURITIUS [S.E.O. NO. 12-Q.1] 1955-1956

DIAPIAQ	[SEQ ID NO:1]	AG..G.....	6.	6.
DIAPIFL	[SEQ ID NO:2]	.....	6.	6.
DIAPIPR	[SEQ ID NO:3]	GA.....	6.	A.

MAJORITY ACCGGACCTTCTGGCCCTGAGGGCCTAACGGCIT

DNAPIAQ	CA.	G.	G.	140
DNAPIFL	T.	C.	C.	137
DNAPTIN			G.	140

MAJORITY 5'-GGCCAAAGAGGCTTCCCTAAGGCCCTGAAGGAGGAACGGGACXXGGGGTGXTGGTCITGACGCCAAG

DNAPTAQ	C.....	A.....	A.....	207
DNAPTFL	A.....	A.....	T.....	204
DNAPTF	A.....	A.....	T.....	210

ONNAPTAO  
ONNAPTFI  
ONNAPTTI

NAPIAO	A.	6	6	6	6	6	6	347
NAPIAII		T	A.	C.	T	G.	G.	344
NAPIAIII						T	T	350

**FIG. 2B**

MAJORITY [SEQ ID NO:7] C8AGCCGACACTGCCACCTGGCAGAGGCGGAAATAAAGGGGGTACAGGTGGCCATCCCT

MAJORITY            AGGGCCGAAACGGGACCTCTACAGGCCTTTCACCCGATGGGCTCCTCCCCAGGGTACCTCA

DNAADPTER . . . . . MAJORITY GAGTGGGGGACCCCTGGAAAACCTCAGAACCTGGACCCCCGTGAAGCCCCC... CXTCCCCGGAGAAAGA  
TC . . . . . A . .

UNAPTAQ	GG.	G.	A.	694
UNAPTFL	T.	C.	A.	691
UNAPTTM	A.	A.	A. AAAA.	700

**FIG. 2C**

MAJORITY [SEQ ID NO:7] TCCAGCCCCACATGAXGACCTGAXGGCTCTCTGGAGCTXTCCGAGGTGGCGACCCGCTGCCGA	764							
DNAPTAG [SEQ ID NO:1] .....	A.....	C.....	T.....	A.....	C.....	GG..	A.....	.....
DNAPTFL [SEQ ID NO:2] .....	GGG.....	G.....	CCC.....	T.....	C.....	A.....	T.....	.....
DNAPTTA [SEQ ID NO:3] .....	A.....	C.....	A.....	C.....	G.....	T.....	C.....	G.....
MAJORITY CGTGGACTTGCCCCAACGXGGGGAGCCCCAACCGGGAGGGGCTTAAGGGCTTTCGGAGAGGCTGAGCTTGAGCTT	765							
DNAPTAG .....	AA.....	.....	.....	A.....	.....	.....	.....	.....
DNAPTFL .....	GG.G.C.C.	CACA.....	A.....	T.....	GC.....	T.....	C.....	.....
DNAPTTA .....	G.....	G.....	.....	.....	.....	.....	G.....	.....
MAJORITY CCCACCCCTGCTCACGAGTTGGCCCTGGAGGGCCCAAGGGCCTGGAGGCCCCCTGGCCGCCGCC	834							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	A.....	.....	.....	.....	.....	.....	.....	.....
DNAPTTA .....	.....	.....	.....	.....	.....	.....	.....	.....
MAJORITY CGGAAAGGGCCCTTCCCTGGCTTTCGGCCGGACCCGATGTGGCCGAACTTCGGCCCTGGC	835							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	A.....	.....	.....	.....	.....	.....	.....	.....
DNAPTTA .....	.....	.....	.....	.....	.....	.....	.....	.....
MAJORITY CGGGCGAGGGGGGGCTCCACGGGGACCCGACGGCTTAXGGGACCTXAGGAGGTG	904							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	A.....	.....	.....	.....	.....	.....	.....	.....
DNAPTTA .....	.....	.....	.....	.....	.....	.....	.....	.....
MAJORITY CGGGCGAGGGGGGGCTCCACGGGGACCCGACGGCTTAXGGGACCTXAGGAGGTG	974							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	T.....	T.....	TCT.....	T.....	.....	.....	.....	.....
DNAPTTA .....	.....	.....	.....	.....	G.....	AAA.....	.....	.....
MAJORITY CGGGCGAGGGGGGGCTCCACGGGGACCCGACGGCTTAXGGGACCTXAGGAGGTG	975							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	TGG.....	G.....	CC.....	T.....	A.....	.....	.....	.....
DNAPTTA .....	TG.....	G.....	.....	.....	G.....	GGC.....	.....	.....
MAJORITY CGGGCGAGGGGGGGCTCCACGGGGACCCGACGGCTTAXGGGACCTXAGGAGGTG	1044							
DNAPTAG .....	.....	.....	.....	.....	.....	.....	.....	.....
DNAPTFL .....	C.....	C.....	G.....	T.....	A.....	A.....	.....	.....
DNAPTTA .....	.....	.....	.....	.....	.....	.....	G.....	.....

**FIG. 2D**

**FIG. 2E**

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCCCCCTCCCCACCCXXCTGGGAGGATCCCCCTTCTGGGCCAGGGAGGCTT	C.	1814
DNAPTAQ [SEQ ID NO:1]	.....	.....	.....
DNAPFL [SEQ ID NO:2]	.....	.....	.....
DNAPTH [SEQ ID NO:3]	.....	.....	.....
MAJORITY	GTTCGCGCCCTGGACTATAGCCAGATAAGCTGGGGCTCCTGGCCCAACCTCTGGGGGACGGAGAACCTG	G.	1884
DNAPTAQ	A.....	A.....	1881
DNAPFL	C.....	T.....	.....
DNAPTH	.....	.....	.....
MAJORITY	ATCCGGGTCTTCAGGAGGGGGAGCATCCACACCCAGACGGGAGCTGGATGTTGGCCGTCCCCGGG	G.	1890
DNAPTAQ	.....	.....	.....
DNAPFL	.....	.....	.....
DNAPTH	.....	.....	.....
MAJORITY	AGGCCCTGGACCCCCGATGCCCTGGGGGGCCAAAGACCATCAACTTGCCCCCTAACGGCAATGTCCCC	G.	1954
DNAPTAQ	.....	.....	1951
DNAPFL	.....	.....	.....
DNAPTH	.....	.....	.....
MAJORITY	CCACCCGCTCTGGGAGGCTTGGCATGCCCTAGGAGGGGGGTGCCCTCATGGCCCTACTTCCAG	G.	1960
DNAPTAQ	.....	.....	.....
DNAPFL	.....	.....	.....
DNAPTH	.....	.....	.....
MAJORITY	.....	.....	2024
DNAPTAQ	.....	.....	2021
DNAPFL	.....	.....	2030
DNAPTH	.....	.....	.....
MAJORITY	.....	.....	2094
DNAPTAQ	.....	.....	2091
DNAPFL	.....	.....	.....
DNAPTH	.....	.....	2100

FIG. 2G

## FIG. 2H

MAJORITY [SEQ ID NO:7] GCGCCCTGGAGGATGGGGGGGGACTGGCTCTGGGCAACGACTAG

DNAPTAQ [SEQ ID NO:1]	A.....	GA 2499
DNAPTF1 [SEQ ID NO:2]	CC.....	.. 2496
DNAPTFH [SEQ ID NO:3]	.....1.	..... GT .. 2505

## FIG. 3A

MAJORITY [SEQ ID NO:8] MXXAMLPLFEPKGRVLLVQGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLIKALKFGD. DAXXUVFDAK

TAQ PRO	[SEQ ID NO:4]	R.G.	.....	H.	.....	69
TFL PRO	[SEQ ID NO:5]	.....	.....	V. V.	.....	68
TTH PRO	[SEQ ID NO:6]	E.	.....	YK. F.	.....	70

MAJORITY APSFRHEAYEAYKAGRAPTIPEDFPROALI|KELVUDLIGLYRFEADDVLTALLAKKAEEKEYEVRIIL

TAQ PRO	.....	GG.	.....	A.	.....	S.	.....	139
TFL PRO	.....	.....	.....	V.	.....	F.	.....	138
TTH PRO	.....	.....	.....	F.	.....	A.	.....	140

MAJORITY TADRDLYQLLSDRIAVILHPEGYLITPAWLWEKYGLRPEQWVSDYRALXGDPDSNLPGVKGI|GEKTAXKLX

TAQ PRO	.....	K.	.....	H.	.....	D.	A.	I.	E.	.....	R.	.....	E.	209
TFL PRO	.....	.....	E.	I.	.....	Y.	.....	A.	I.	.....	QR.	I	R.	208
TTH PRO	.....	.....	V.	V.	.....	H.	....	F.	V.	.....	L.	..	K.	210

MAJORITY EWGSLENLKLHLDVKP. XXREKIXAHMEDLXLSXVXRTDOLPLEVDAXRREPDRERLIEREF

TAQ PRO	.....	A.	.....	AI.	.....	WD.	AK.	.....	K.	.....	R.	.....	278		
TFL PRO	.....	FOH.	Q.	SL.	.....	LG.	A.	AK.	Q.	H.	.....	GR.	T.	277	
TTH PRO	.....	.....	.....	ENV.	.....	K.	L.	R.	L.	E.	R.	.....	L.	QG.	280

MAJORITY GSLLIHEFGGLEXPKALEFAPWPPEGAFAVGFULSRAPEPMWAELLALAARXGRVHRAXDPLXGIRDLKEY

TAQ PRO	.....	S.	.....	.....	K.	.....	O.	.....	G.	.....	PE.	YKA.	.....	A.	348	
TFL PRO	.....	.....	G.	A.	.....	1.	SF.	.....	Q.	WE.	I.	Q.	R.	.....	G.	347
TTH PRO	.....	.....	.....	.....	.....	.....	AP.	.....	K.	C.	D.	A.	A.	K.	350	

**FIG. 3B**

MAJORITY [SEQ ID NO:8] AGLLAKDIAVLALRFEGIDIXPGODPMIAYLIDPSNTIPGQWARRYGEWEEDAGERALLSERFLFXNLXX

TAQ PRO	[SEQ ID NO:4]	.	S.	.....	G. P.	.....	E. ....	A. ....	A. ....	WG 418
TFL PRO	[SEQ ID NO:5]	.	F.	.....	F.	.....	A. ....	A. ....	QT. KE 417	
TTH PRO	[SEQ ID NO:6]	.	S.	.....	V.	.....	AH. ....	HR. ....	LK 420	

MAJORITY RIEGEERILLWIVYXEVEKPLSRVLAHMEATIGVRLDWAYLQALSLEVAFERBRLEEVFRLAGHPFNLMSRD

TAQ PRO	.	R.	....	R. ....	A.	.....	R. ....	A. ....	A. ....	488
TFL PRO	K.	....	E.	....	R.	.....	EA. V. Q.	.....	.....	487
TTH PRO	.	K. ....	K. ....	.....	H.	.....	L.	.....	.....	490

MAJORITY QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEXILQYRELTKLKNTYIDPLPXLVHPRTG

TAQ PRO	.	.....	DR.	.....	DR.	.....	S. ....	D. I.	.....	558
TFL PRO	.	.....	R. ....	I. ....	C.	.....	H. ....	A. ....	K. ....	557
TTH PRO	.	.....	R. ....	I. ....	C.	.....	H. ....	V. ....	S. ....	560

MAJORITY RLHTTRFNOTATAITGARLSSSDPHLONIPURITPLCQRIRRAFVAEEGWXVALVDYSQIELRVLAHLSGDENL

TAQ PRO	.	.....	I.	....	I.	.....	.....	.....	.....	628
TFL PRO	.	.....	.....	.....	V.	.....	.....	.....	.....	627
TTH PRO	.	.....	.....	.....	A. A.	.....	.....	.....	.....	630

MAJORITY I RVFOEGRDIHTQTASWMFGUPPEAVDPLMRRAAKTIINFQVLYGMSAHLRSQELAI PYEEAVAVAFIERYFO

TAQ PRO	.	.....	E.	....	R.	.....	Q. ....	.....	.....	698
TFL PRO	.	.....	S.	....	G.	.....	G. S.	.....	.....	687
TTH PRO	.	.....	K.	....	V.	.....	.....	.....	.....	700

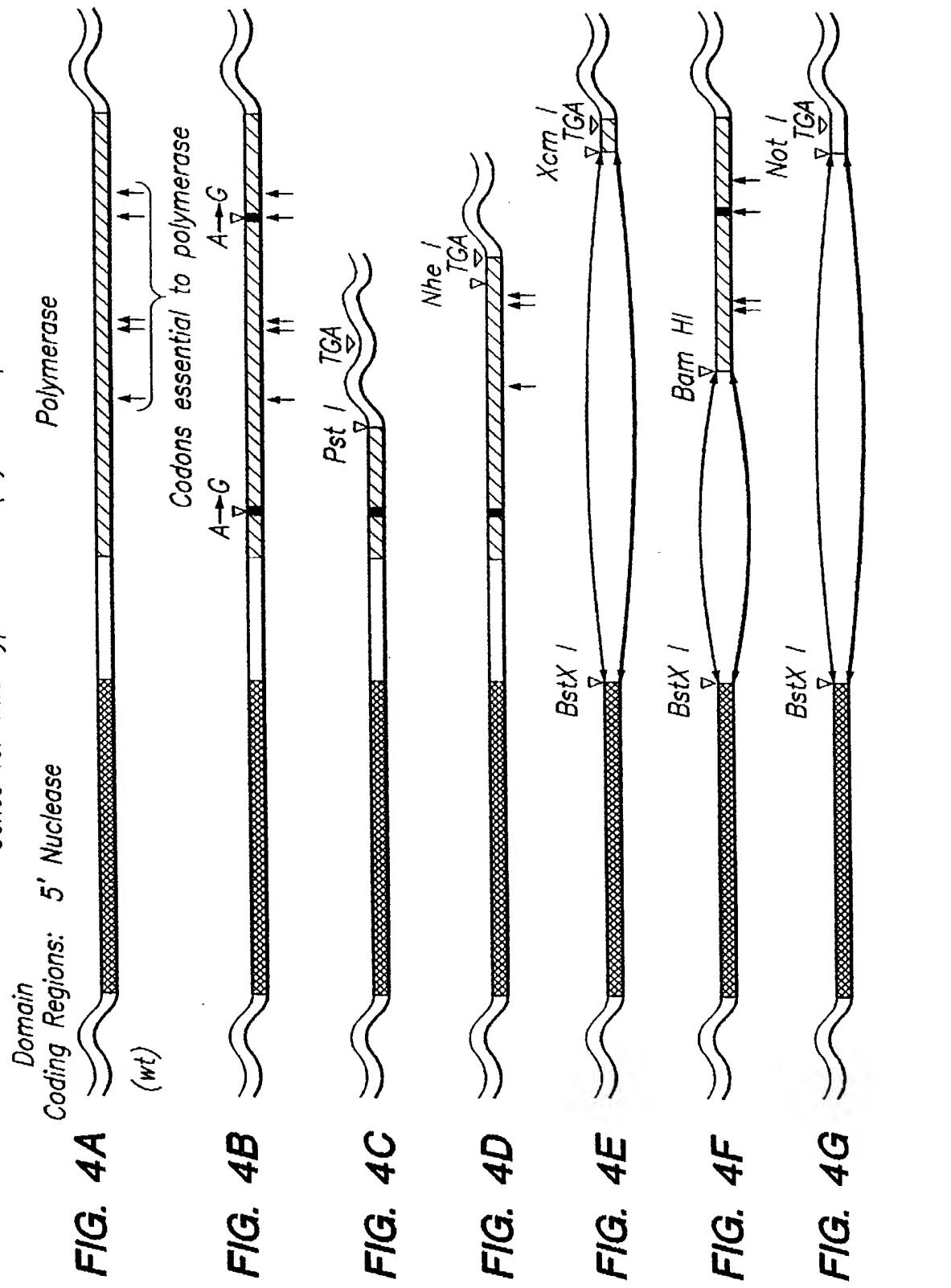
**FIG. 3C**

MAJORITY [SEQ ID NO:8] SFPKVRAWI EKTLFEGRRAGYVETLFCARRRYVPDILNARVKSVREAAERMAFNMPVOGTAADLMKLAMVKL

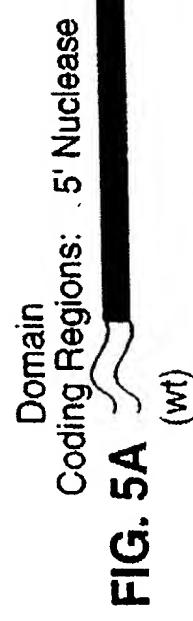
TAQ PRO [SEQ ID NO:4] ..... E.....  
TFL PRO [SEQ ID NO:5] . Y..... G.....  
TTT PRO [SEQ ID NO:6] ..... K.....  
  
MAJORITY FPRLXEMGARMQLQVHDELVLLEAPKXRAEXUAALAKEVMEGVYPLANPLIEVENGGXXGEDDWLSAKEX

TAQ PRO ..... F..... E..... A..... R.....  
TFL PRO ..... Q..... L..... D..... R..... W..... Q.....  
TTT PRO ..... R..... I..... QA..... E..... A..... KA..... M..... G.....  
  
768 ..... E.....  
767 ..... R.....  
770 .....  
  
833 ..... I.....  
831 ..... L.....  
835 ..... M..... G.....

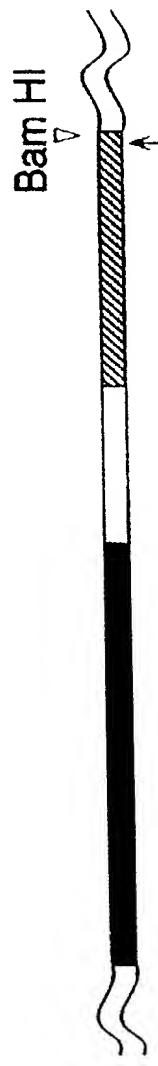
*Genes for Wild-Type and Pol(-)DNAP<sub>Taq</sub>*



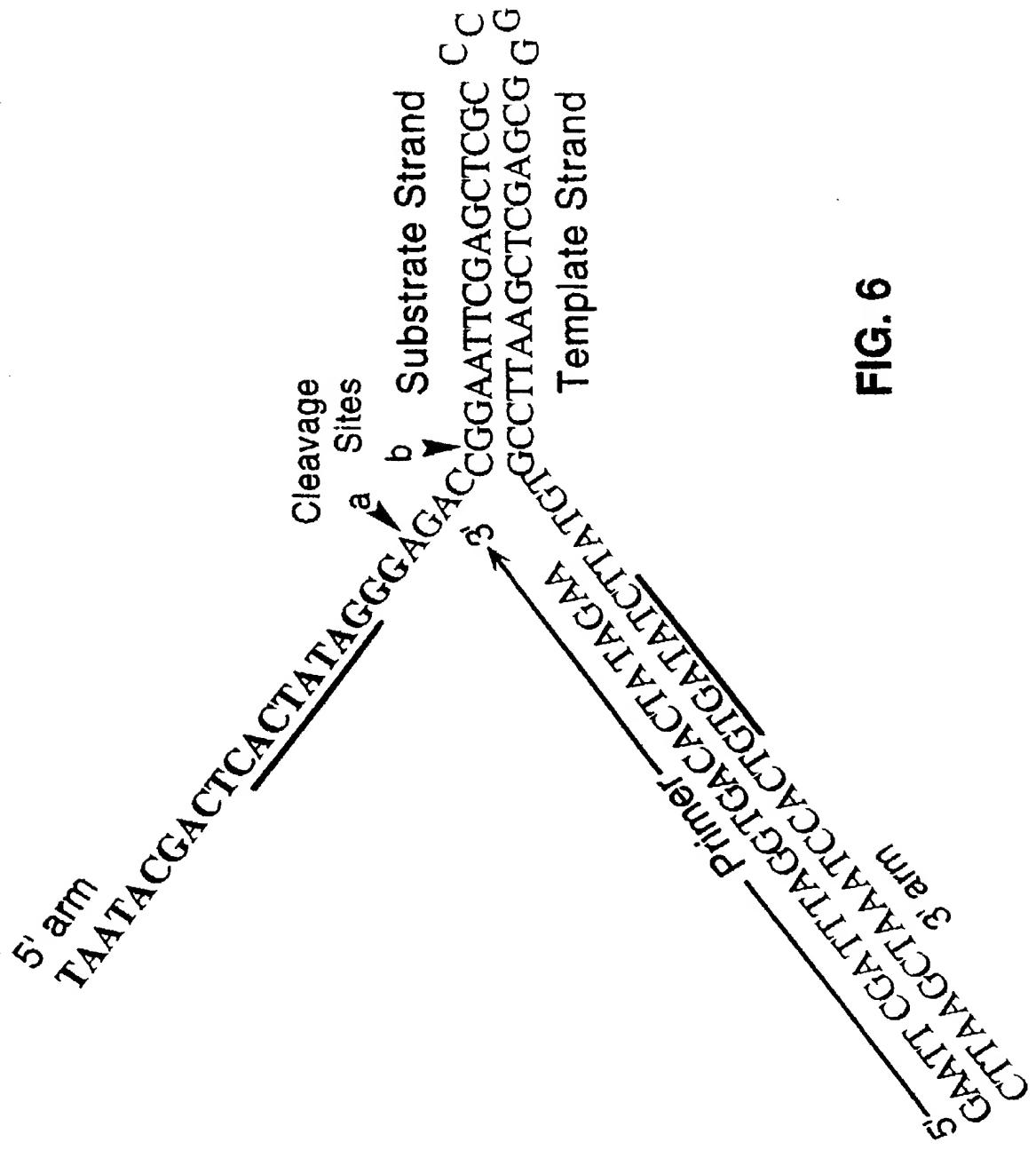
Genes for Wild-Type and Pol(-) DNAPT<sup>fl</sup>



**FIG. 5B**



**FIG. 6**



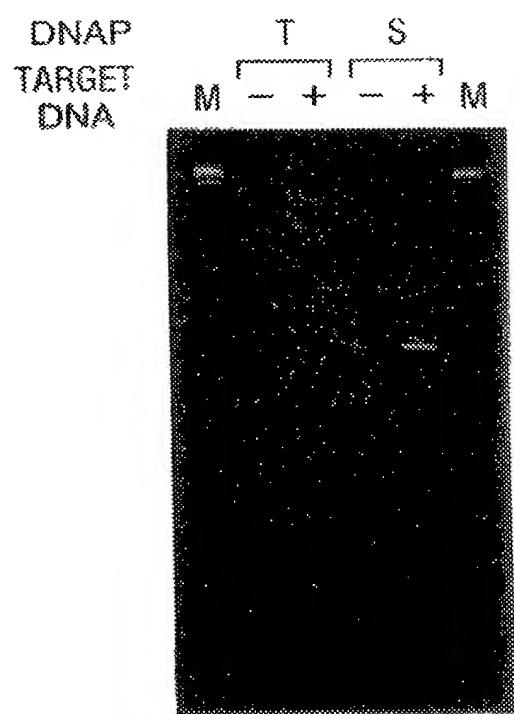


FIG. 7

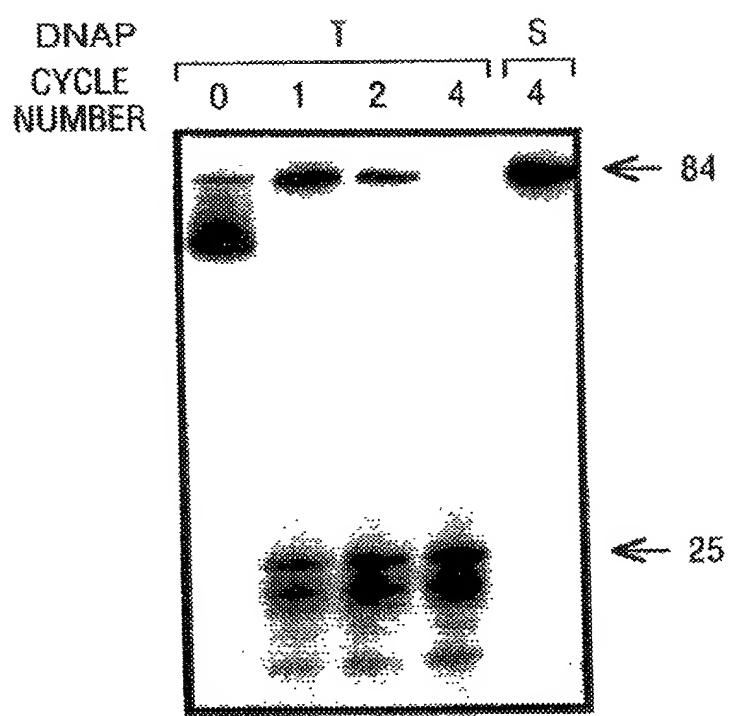
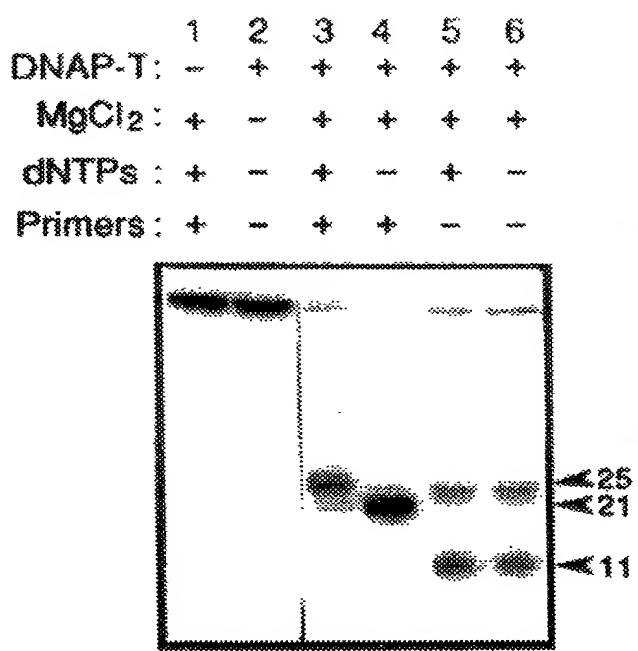
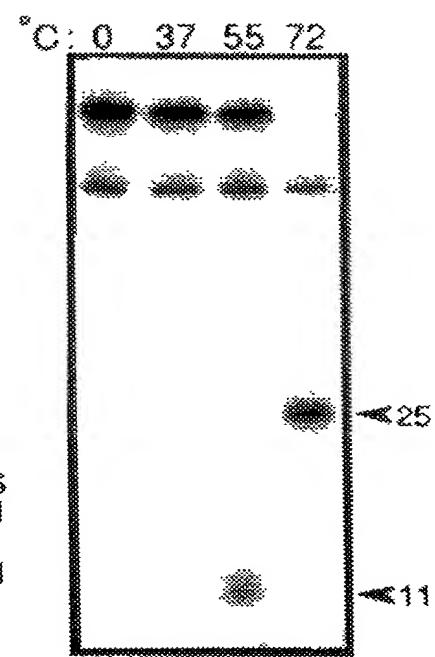


FIG. 8



**FIG. 9A**



**FIG. 9B**

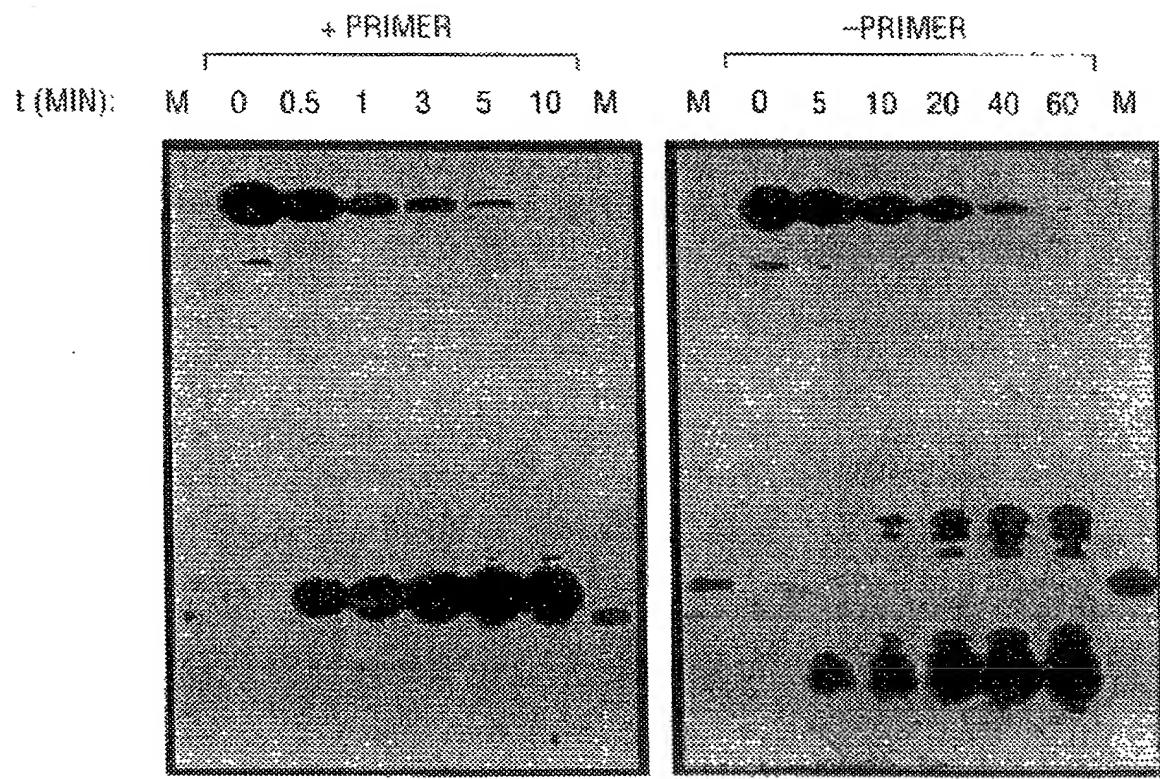


FIG. 10A

FIG. 10B

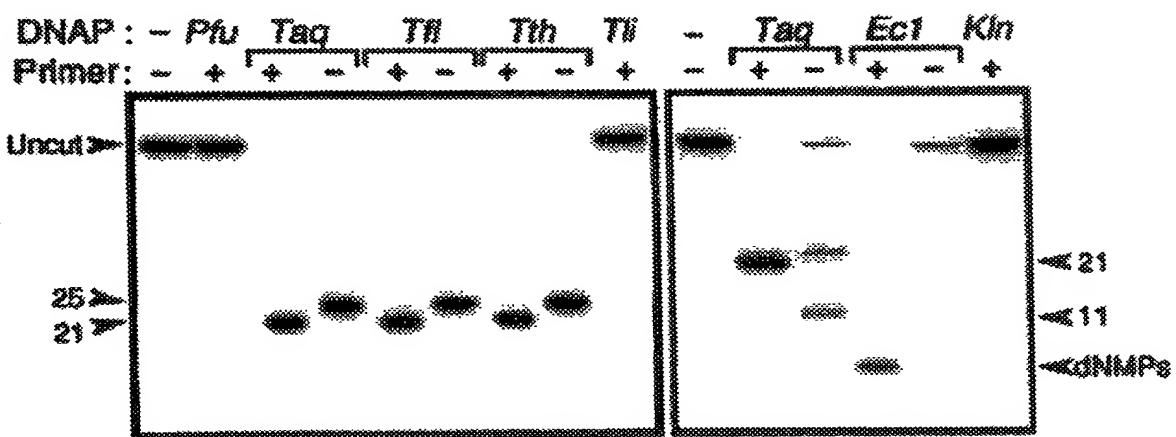
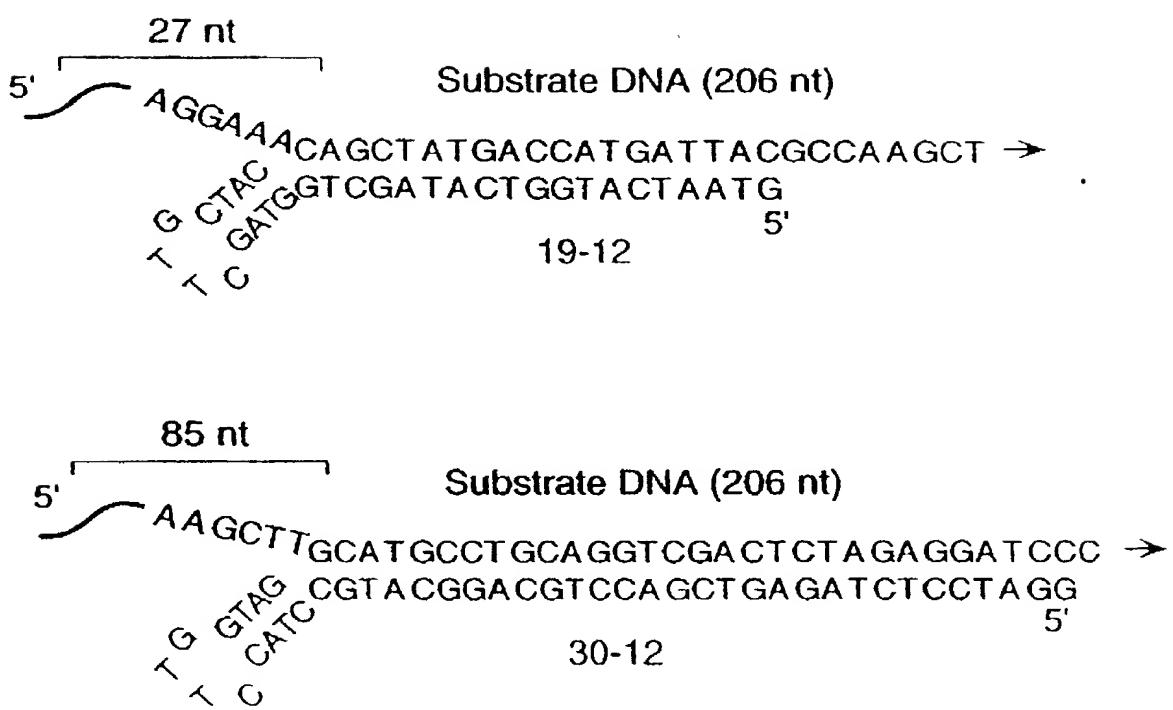
**FIG. 11A****FIG. 11B**

FIG. 12A



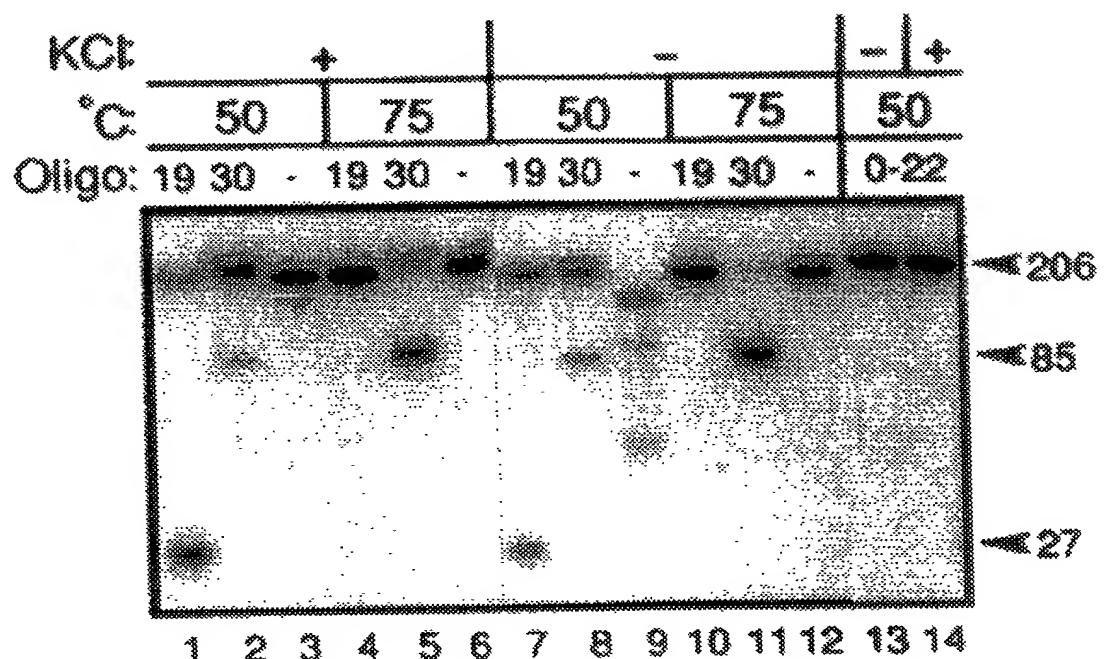


FIG. 12B

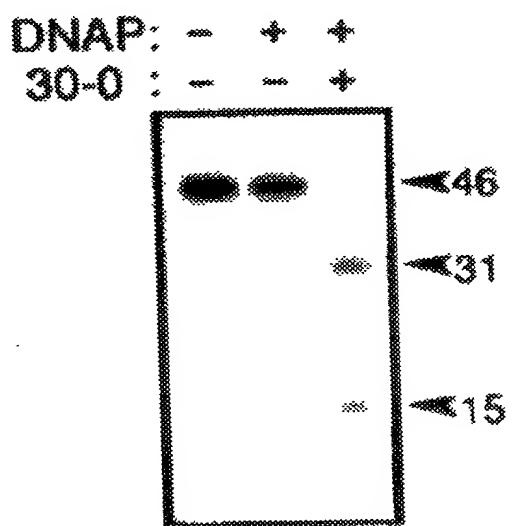
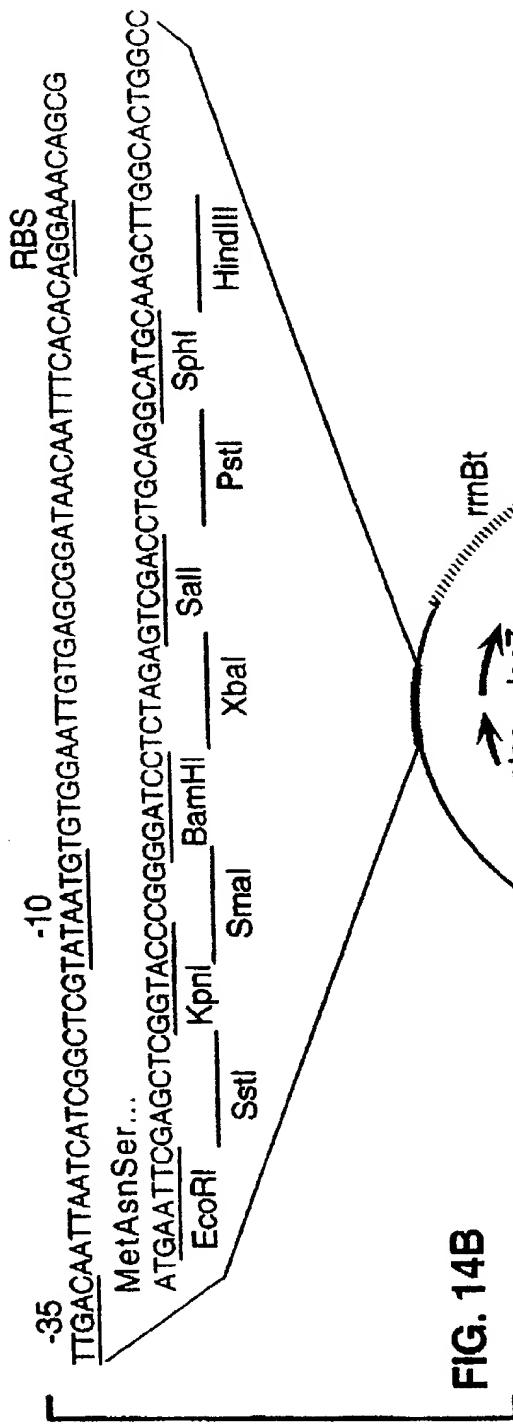


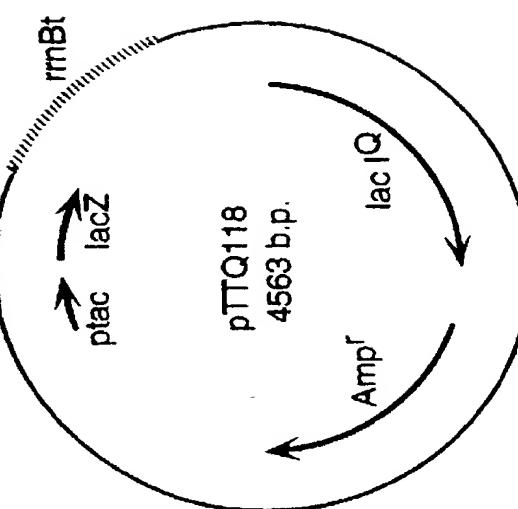
FIG. 13B

15 nt                              Substrate RNA (46 nt)

FIG. 13A



**FIG. 14B**

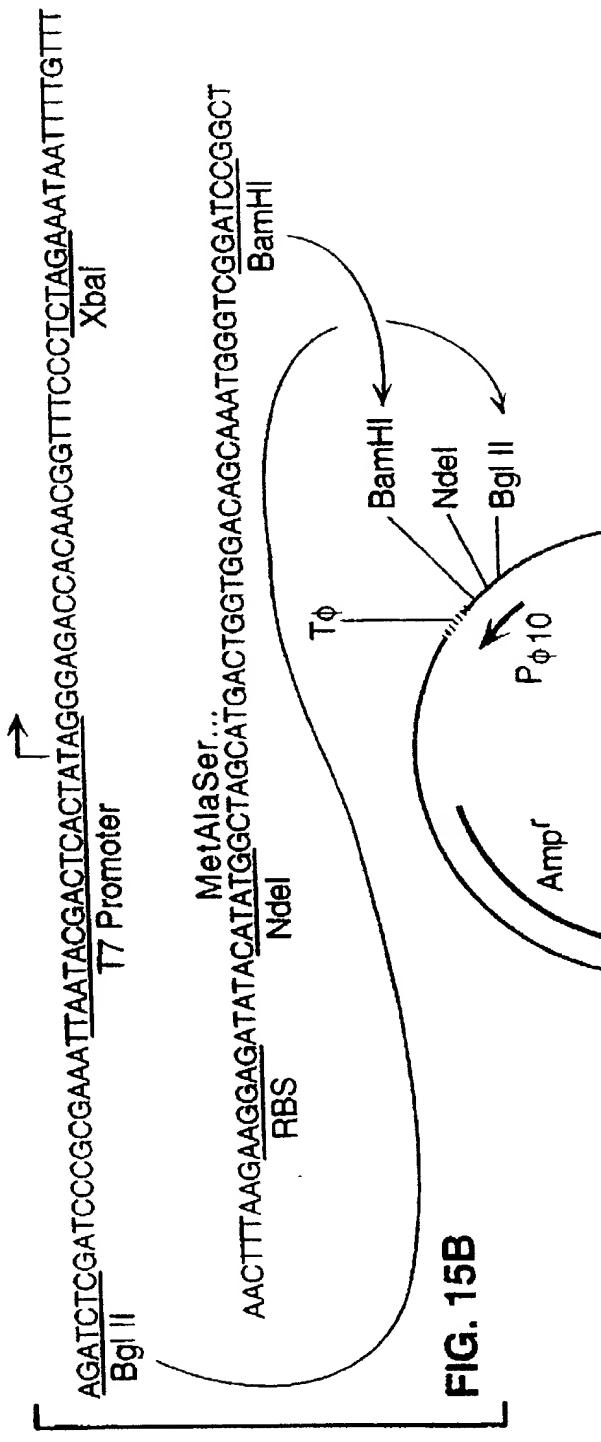


**FIG. 14A**

RBS: Ribosome binding site  
lacZ: Beta-galactosidase alpha fragment  
ptac: Synthetic tac promoter  
lacIQ: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment  
rmBt: E. coli rmB transcription terminator

**FIG. 14C**



**FIG. 15B**

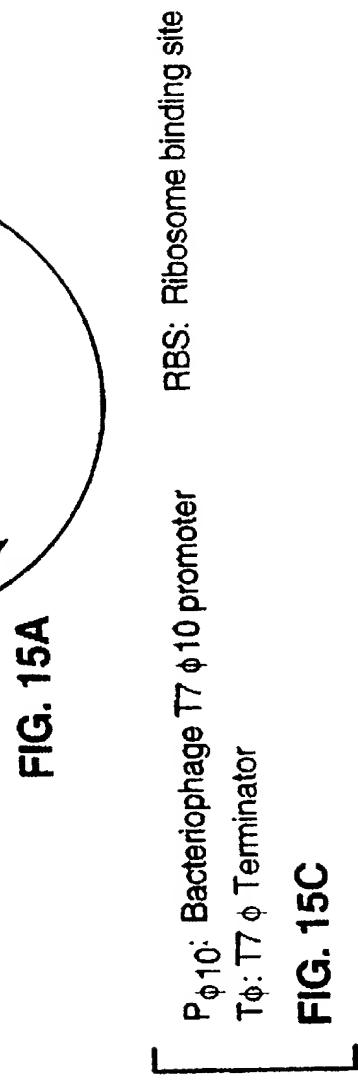
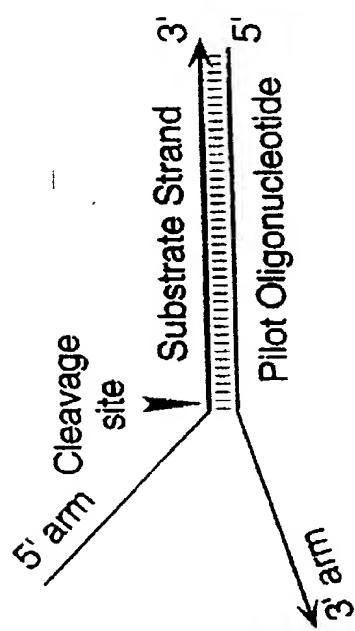
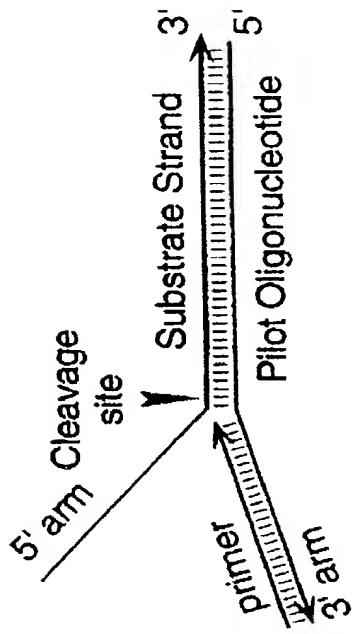


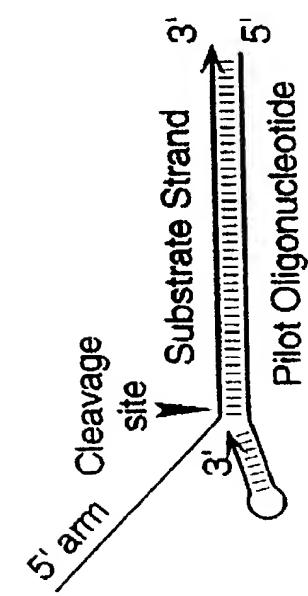
FIG. 15C



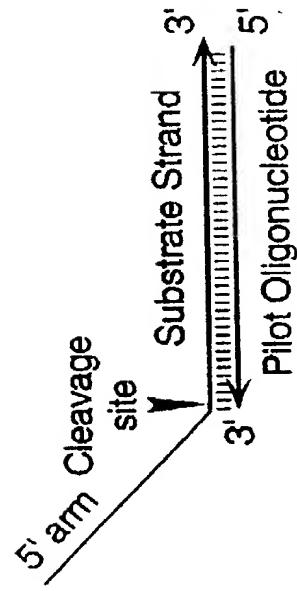
**FIG. 16A**



**FIG. 16B**

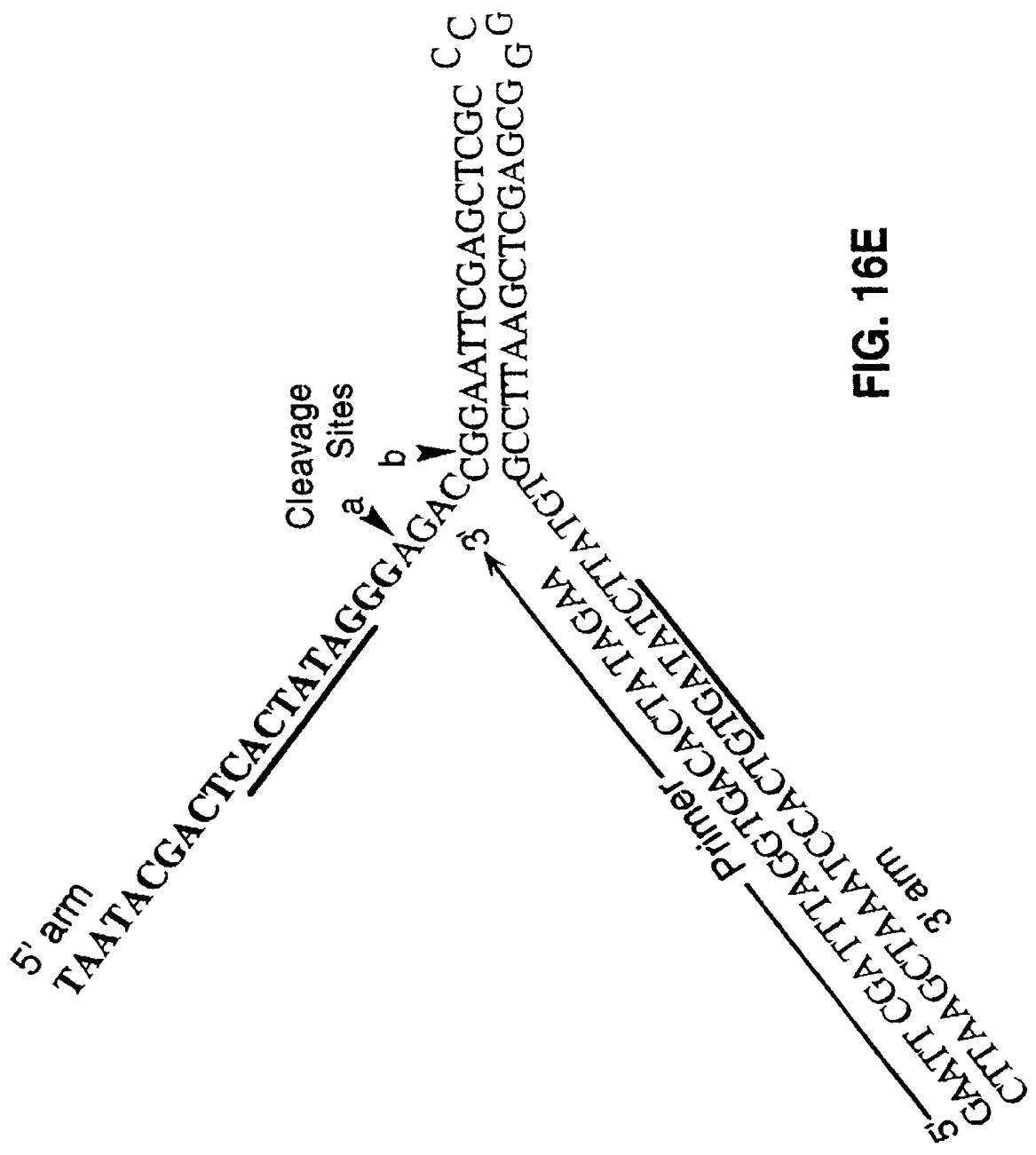


**FIG. 16C**

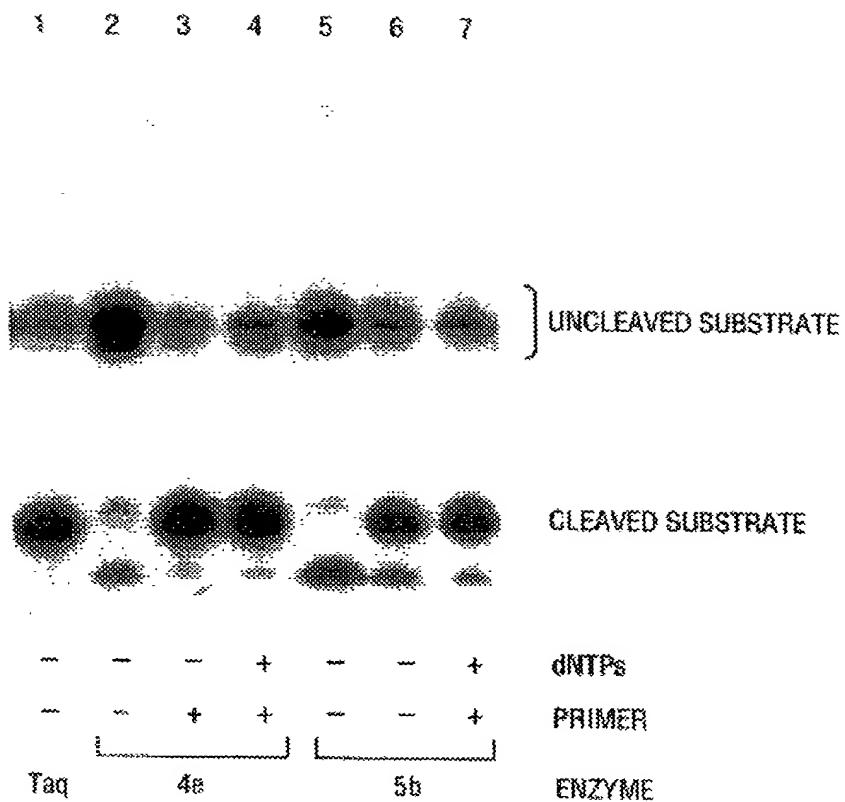


**FIG. 16D**

**FIG. 16E**



**FIG. 17**



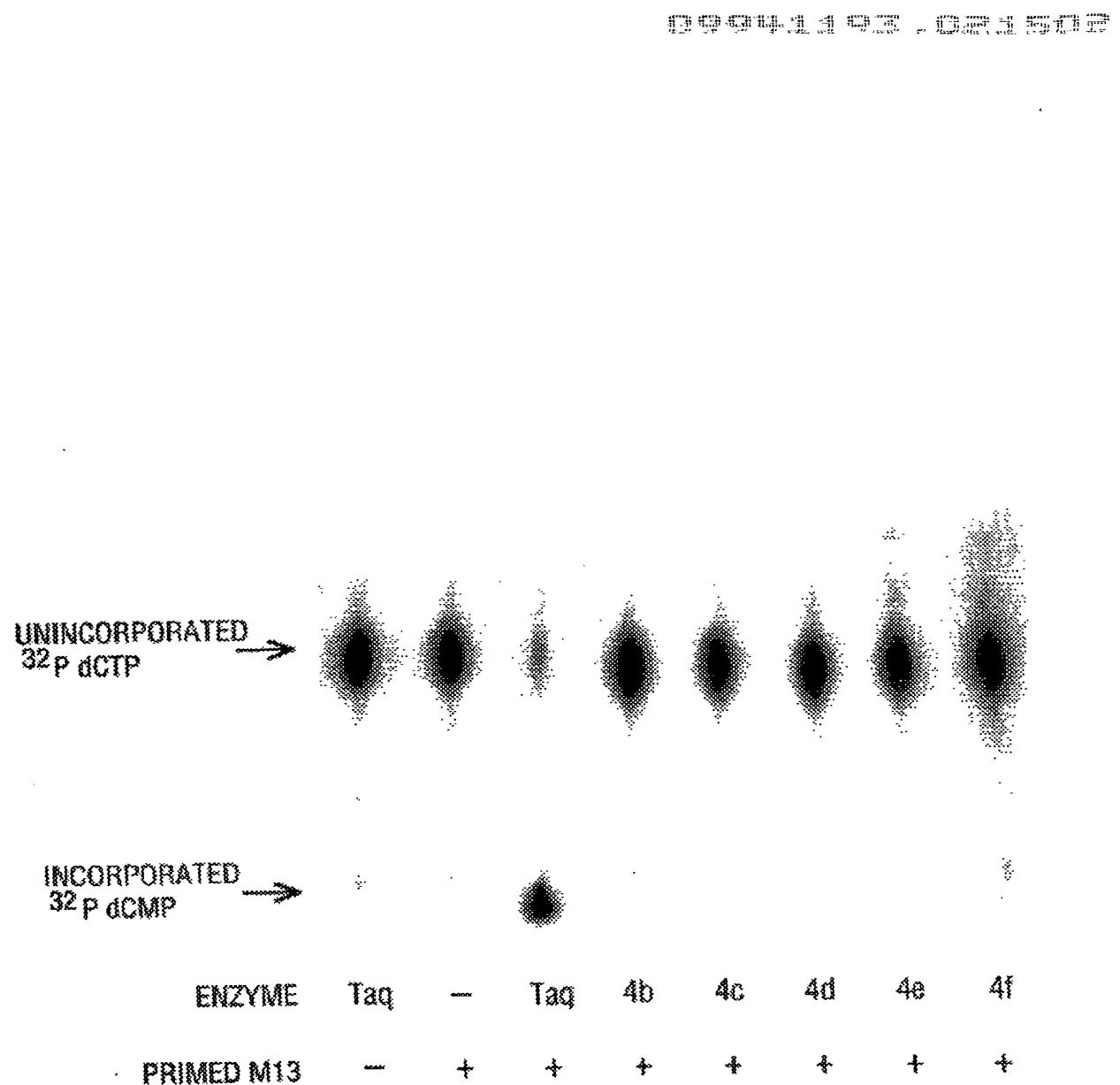
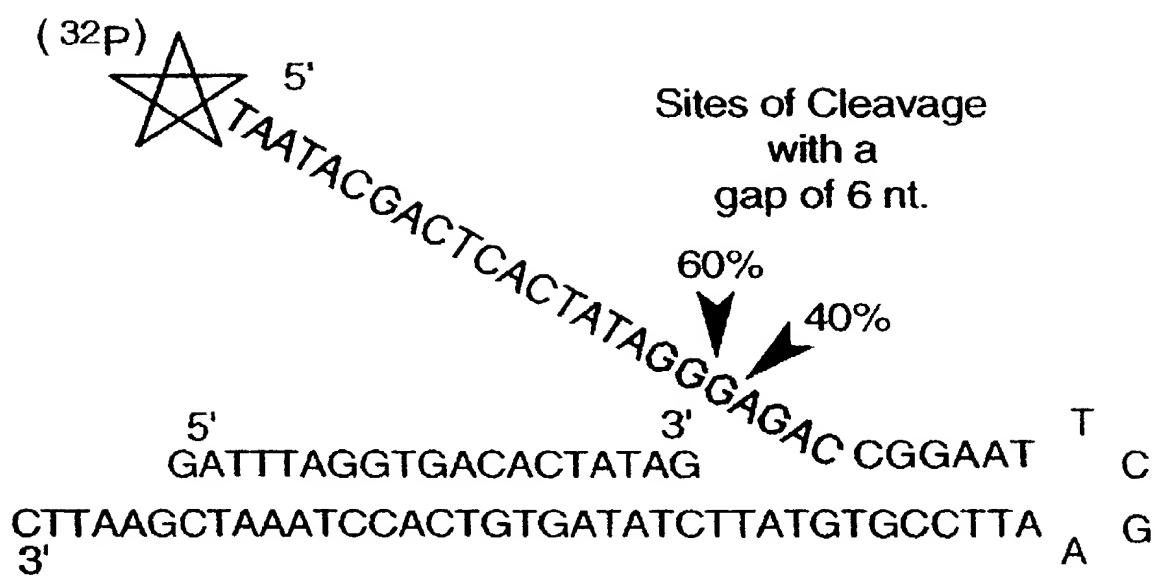


FIG. 18



**FIG. 19A**

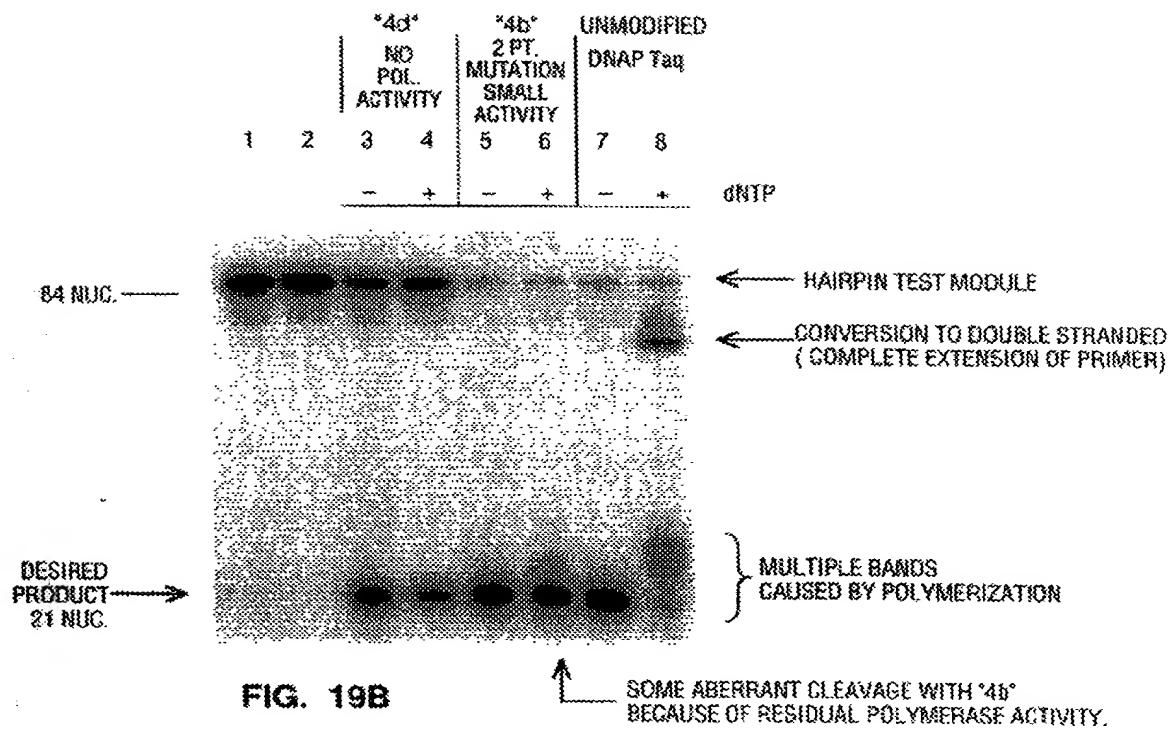
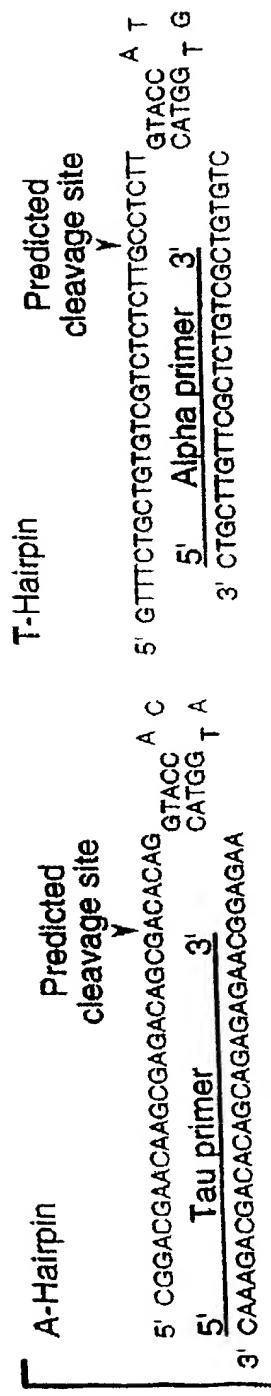


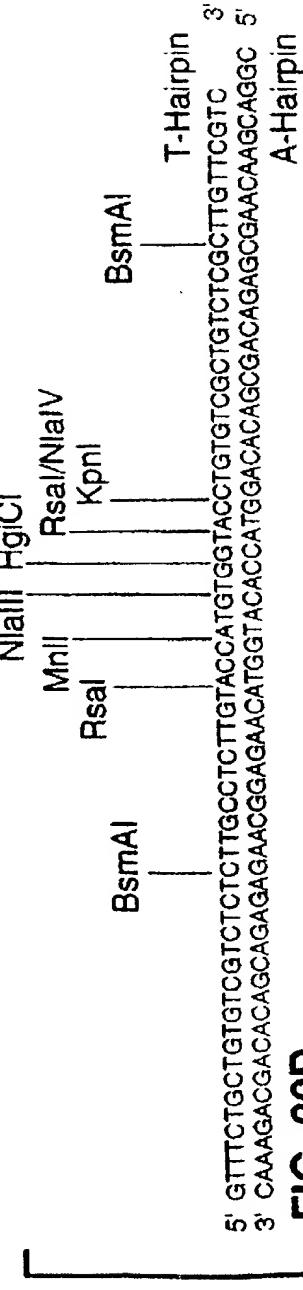
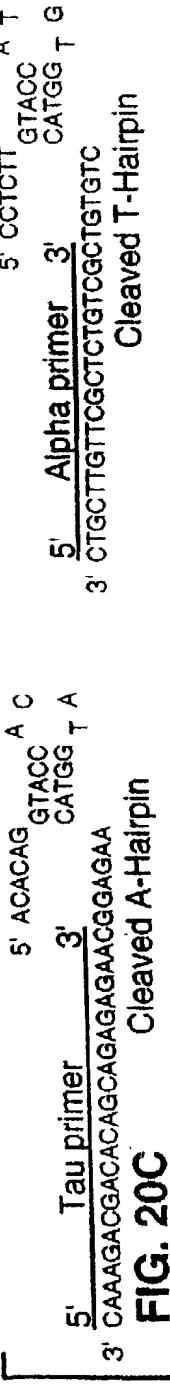
FIG. 19B



**FIG. 20A**

Sequence of alpha primer:  
5' GACGAAACAAGCGAGACAGCACAG 3'

**FIG. 20B**



**FIG. 20D**

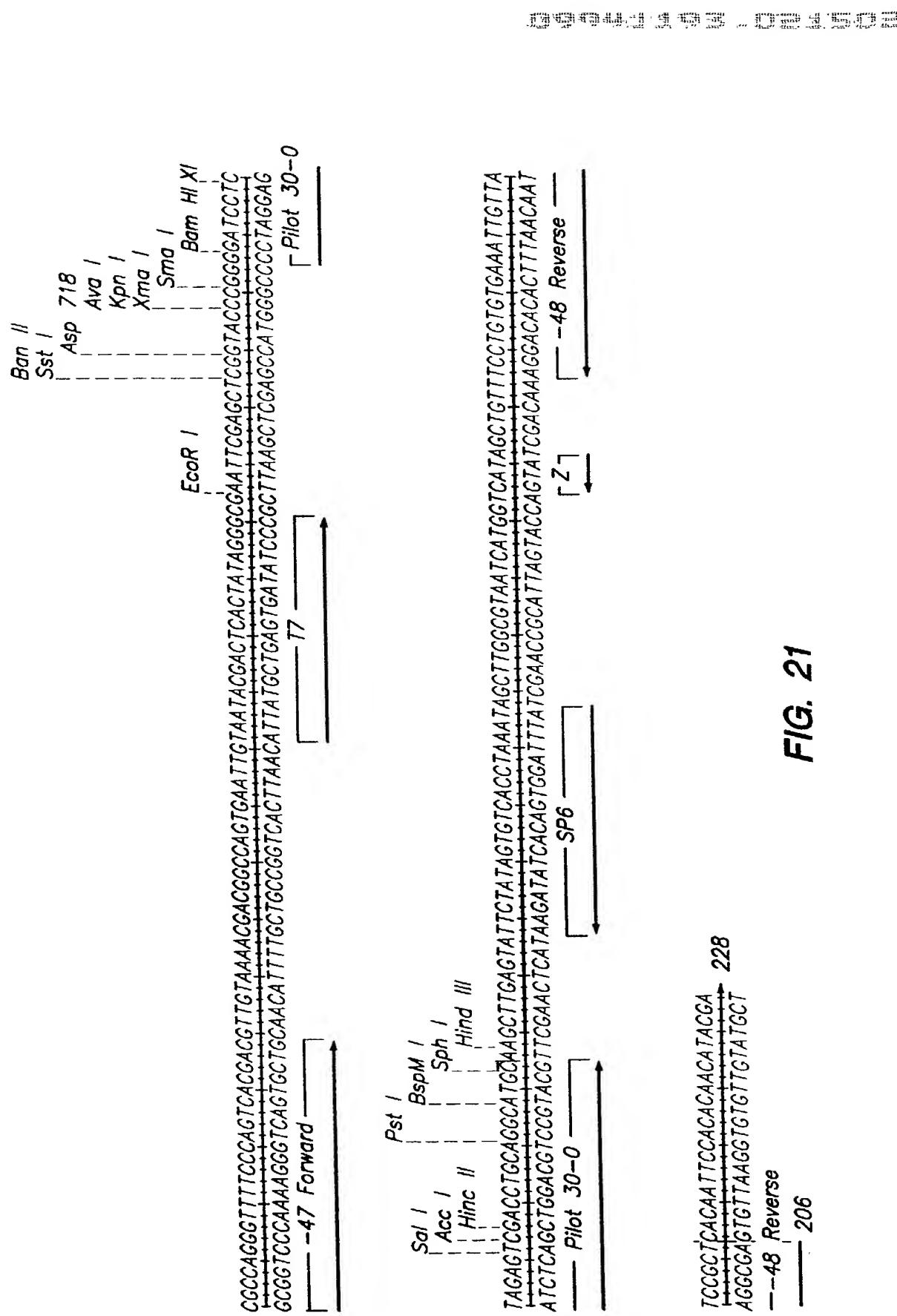
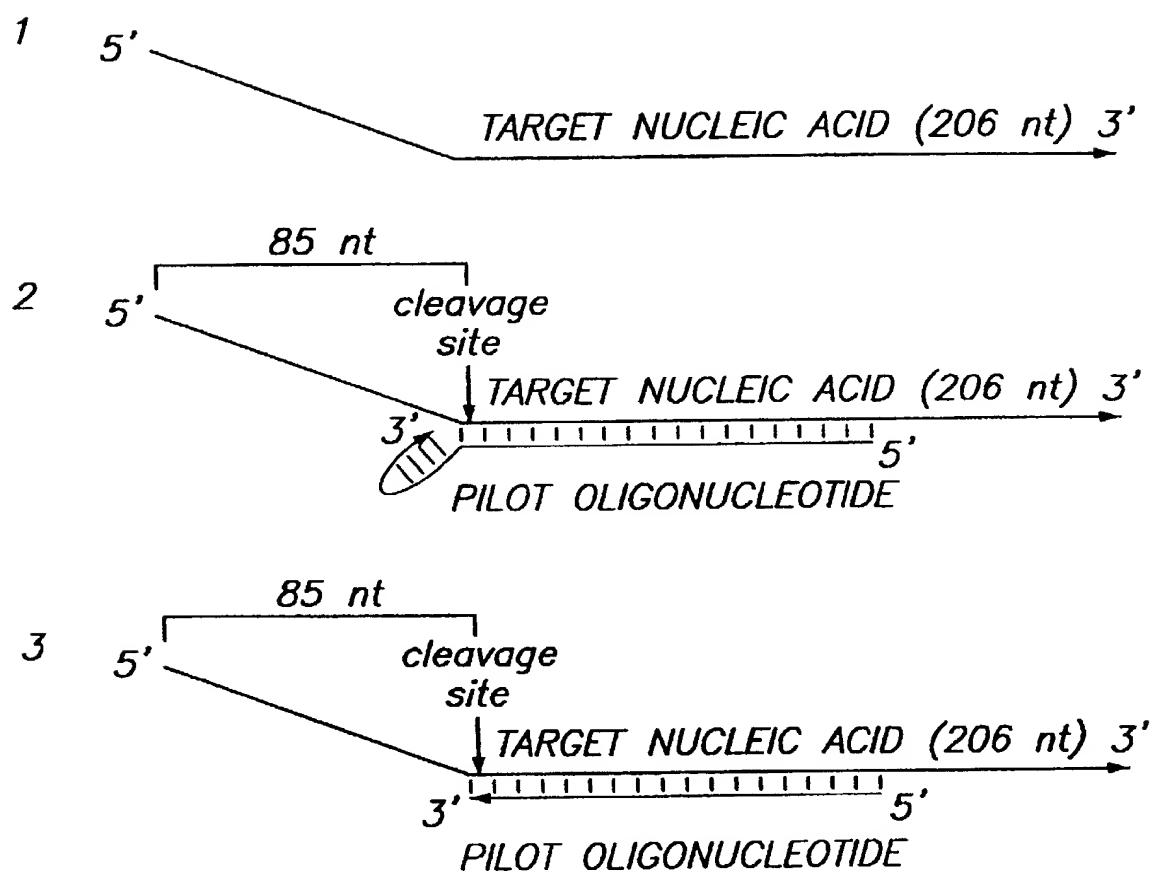


FIG. 21



**FIG. 22A**

THE SO-CALLED "LAW OF DEMAND" IS NOT A LAW OF ECONOMICS

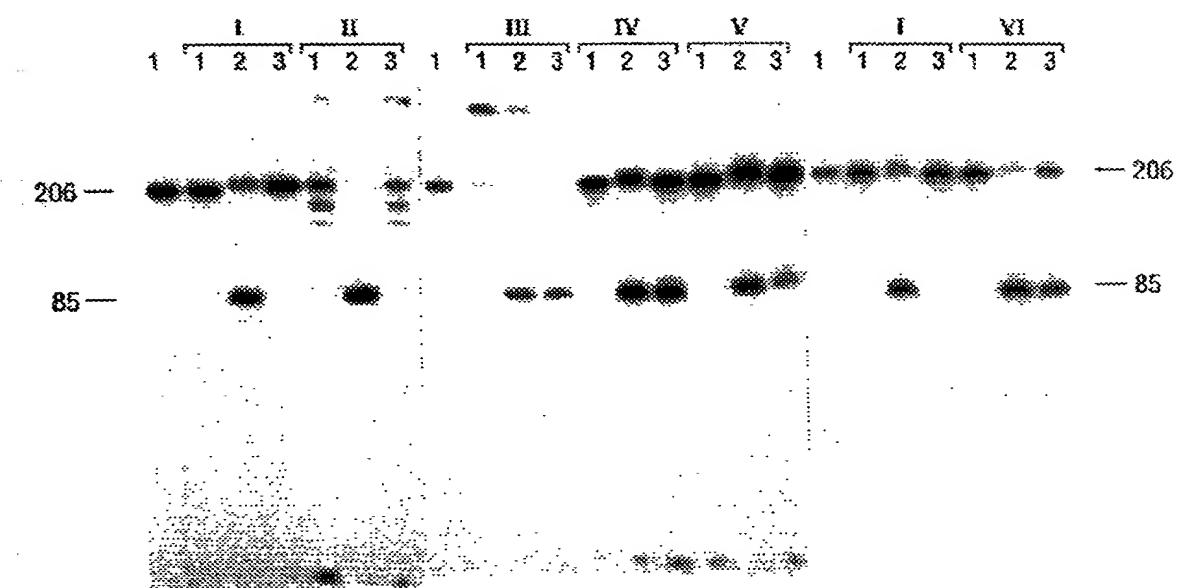


FIG. 22B

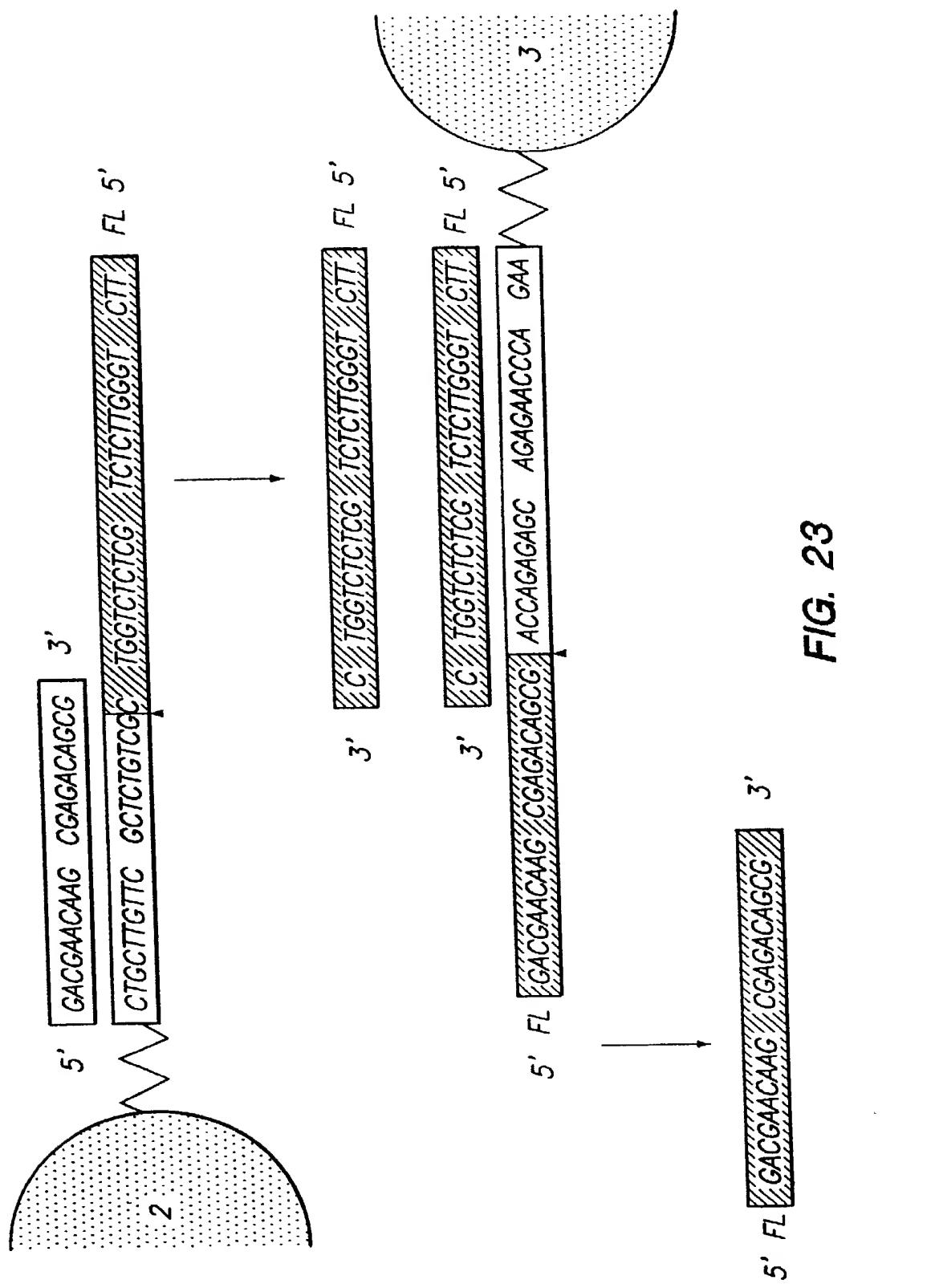


FIG. 23

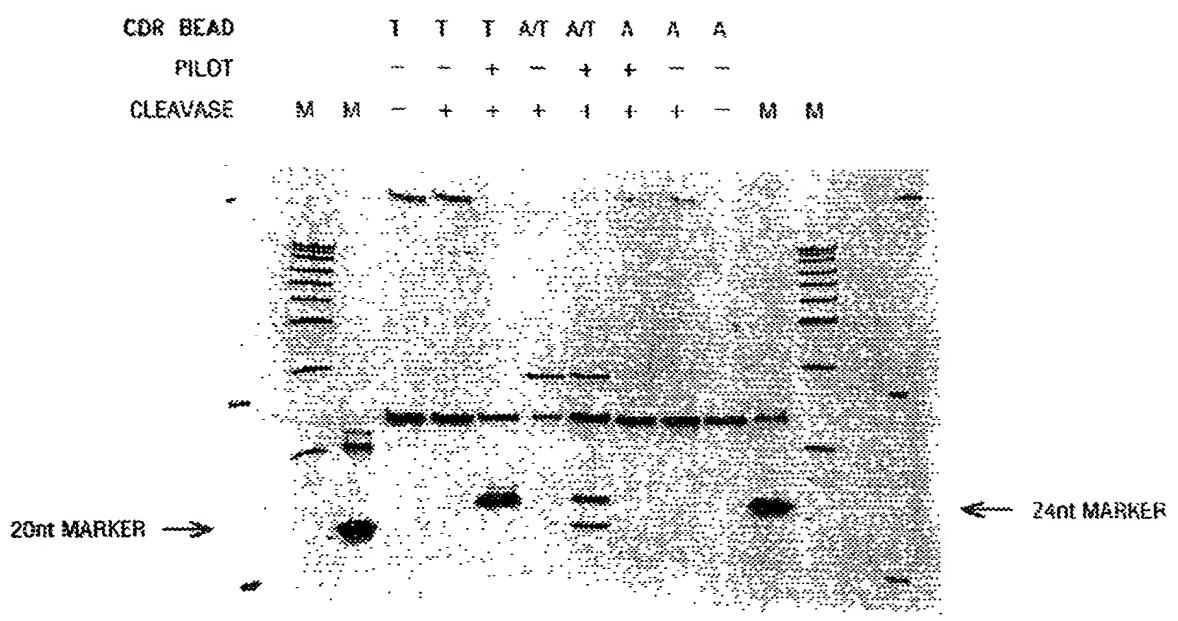
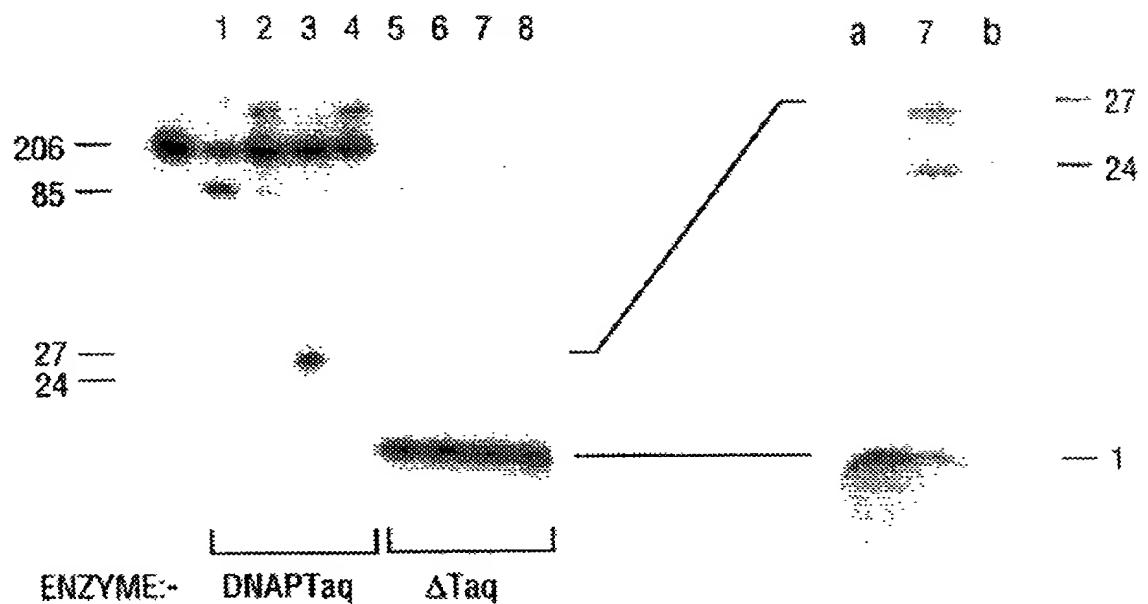
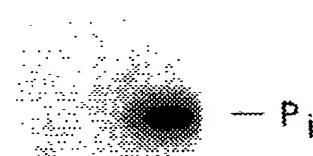


FIG. 24

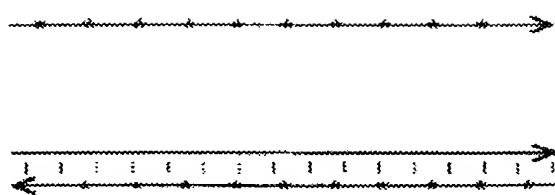


**FIG. 25A**

**FIG. 25B**

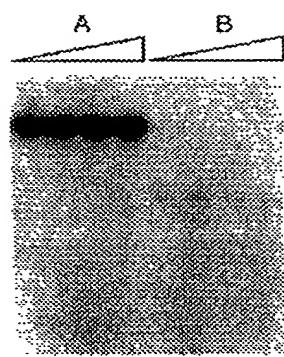


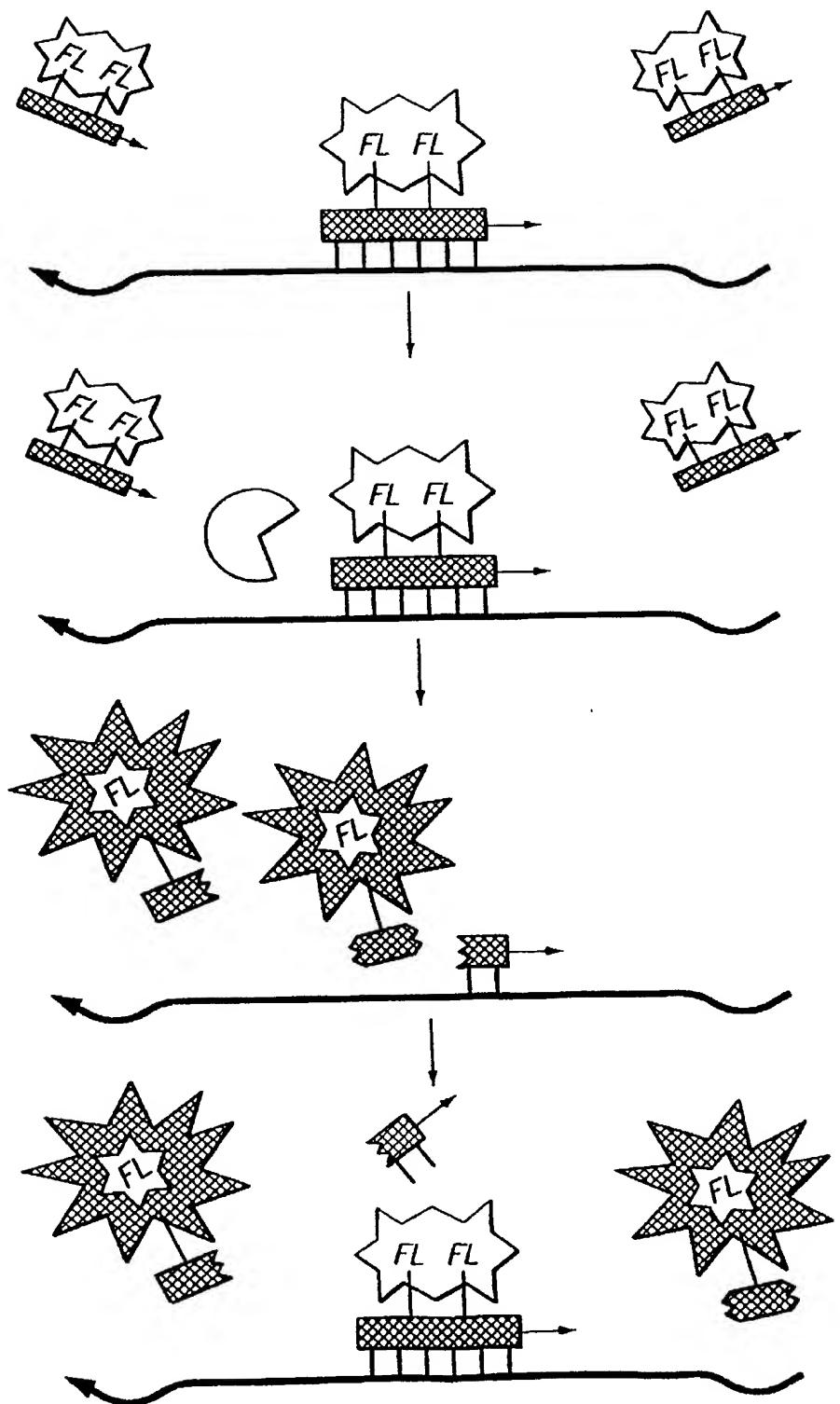
**FIG. 26A**



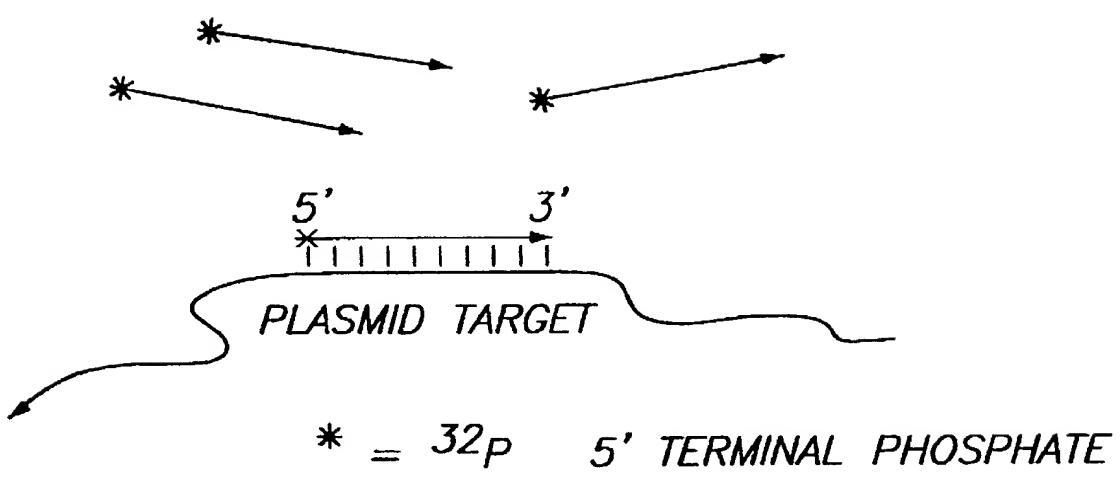
**FIG. 26B**

$\leftarrow \text{ } ^{32}\text{P}$

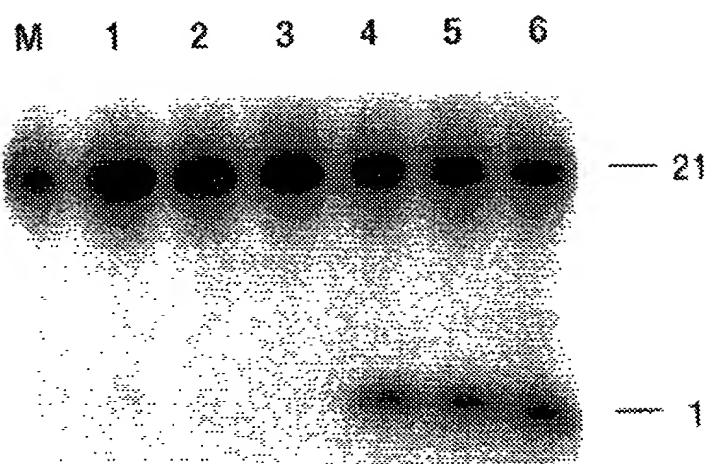




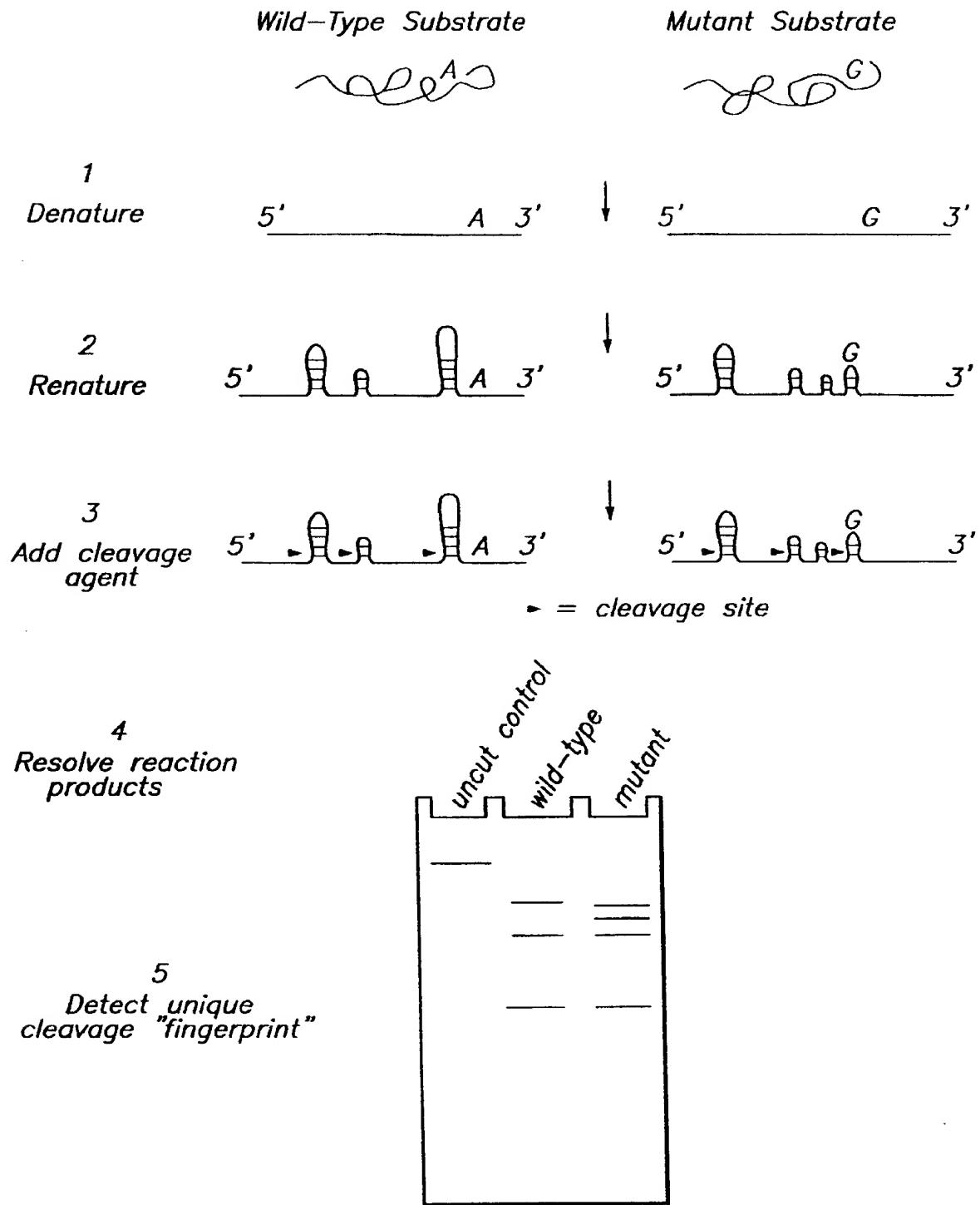
**FIG. 27**



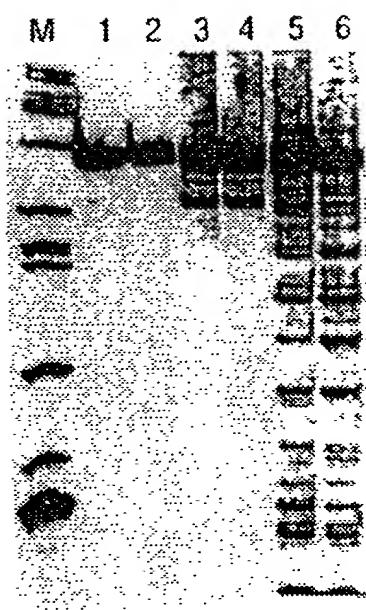
**FIG. 28A**



**FIG. 28B**



**FIG. 29**



**FIG. 30**

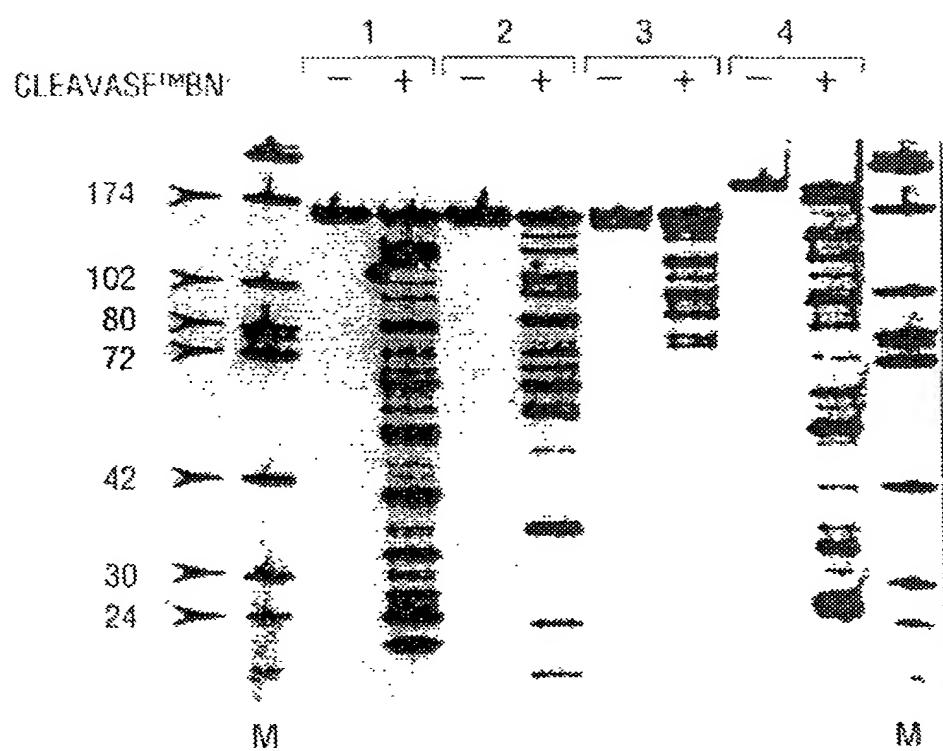
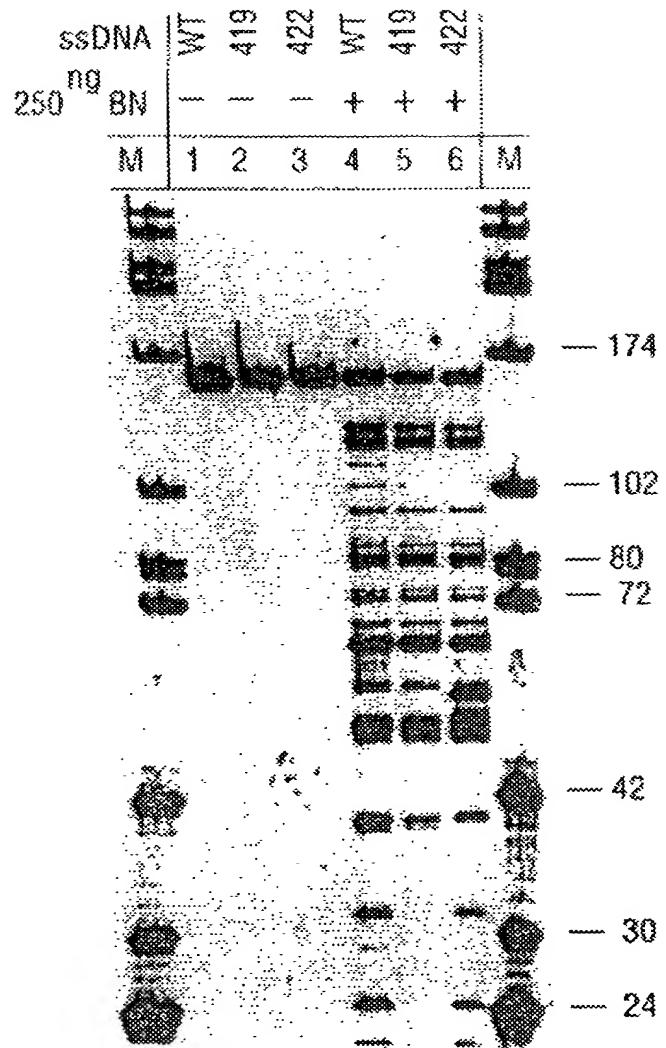


FIG. 31



**FIG. 32**

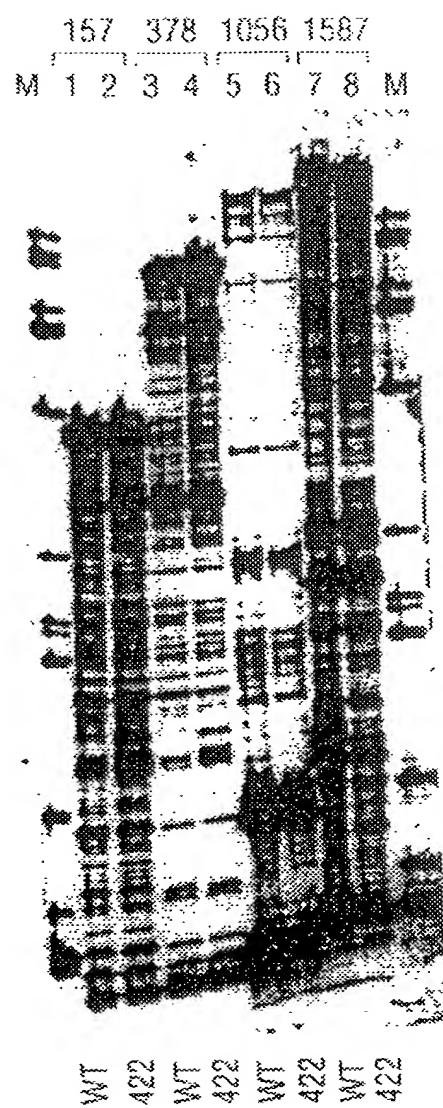
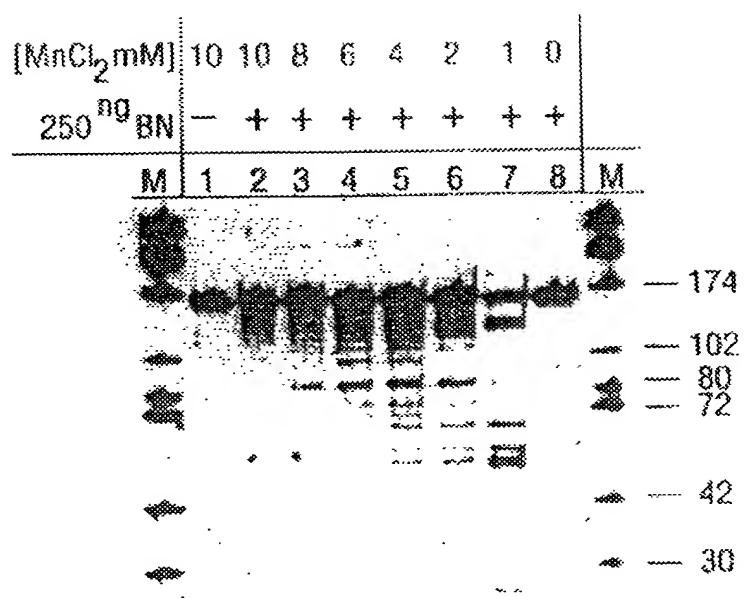


FIG. 33



**FIG. 34**

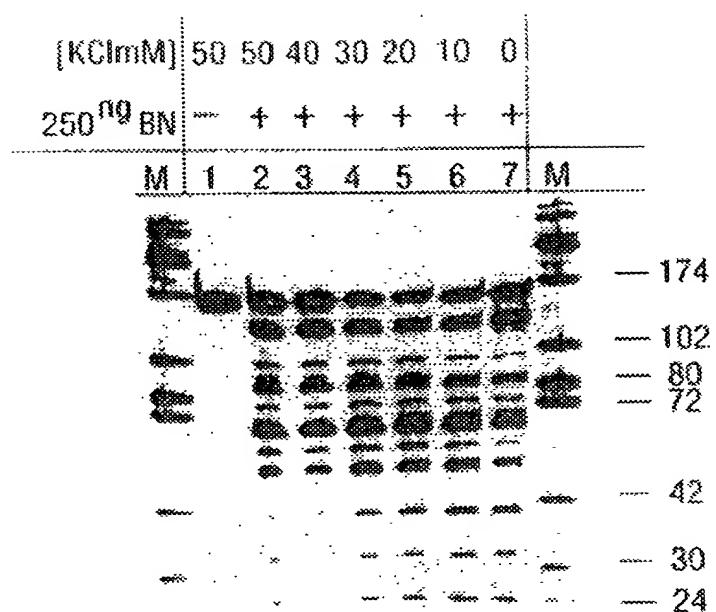


FIG. 35

For more information about the study, contact Dr. John C. Marshall at (301) 435-6310 or

TIME (MIN.)	10	<1	1	5	10
CLEAVASE™BN:	-	+	+	+	?

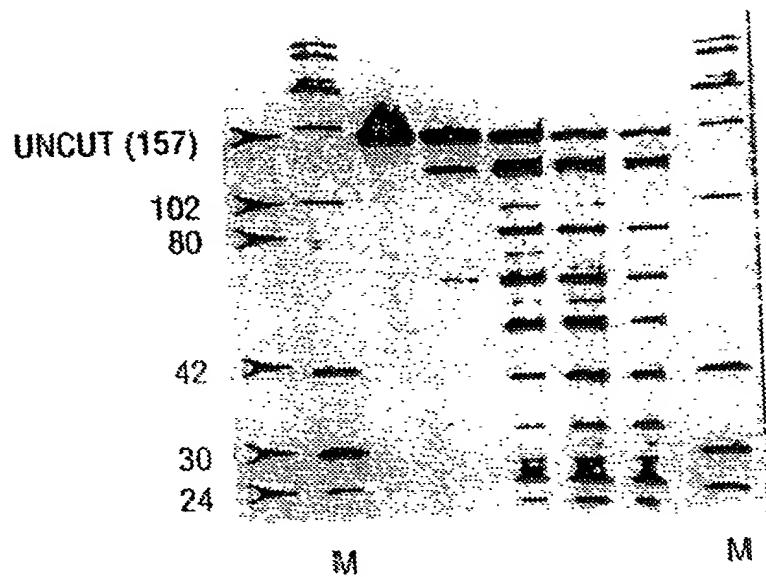


FIG. 36

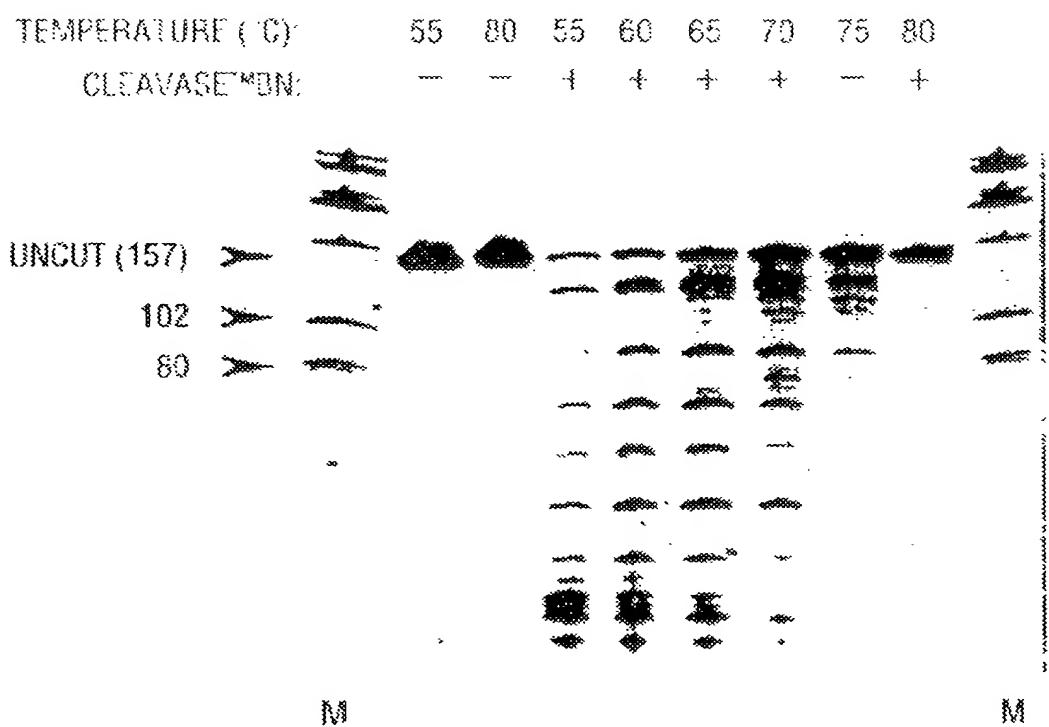
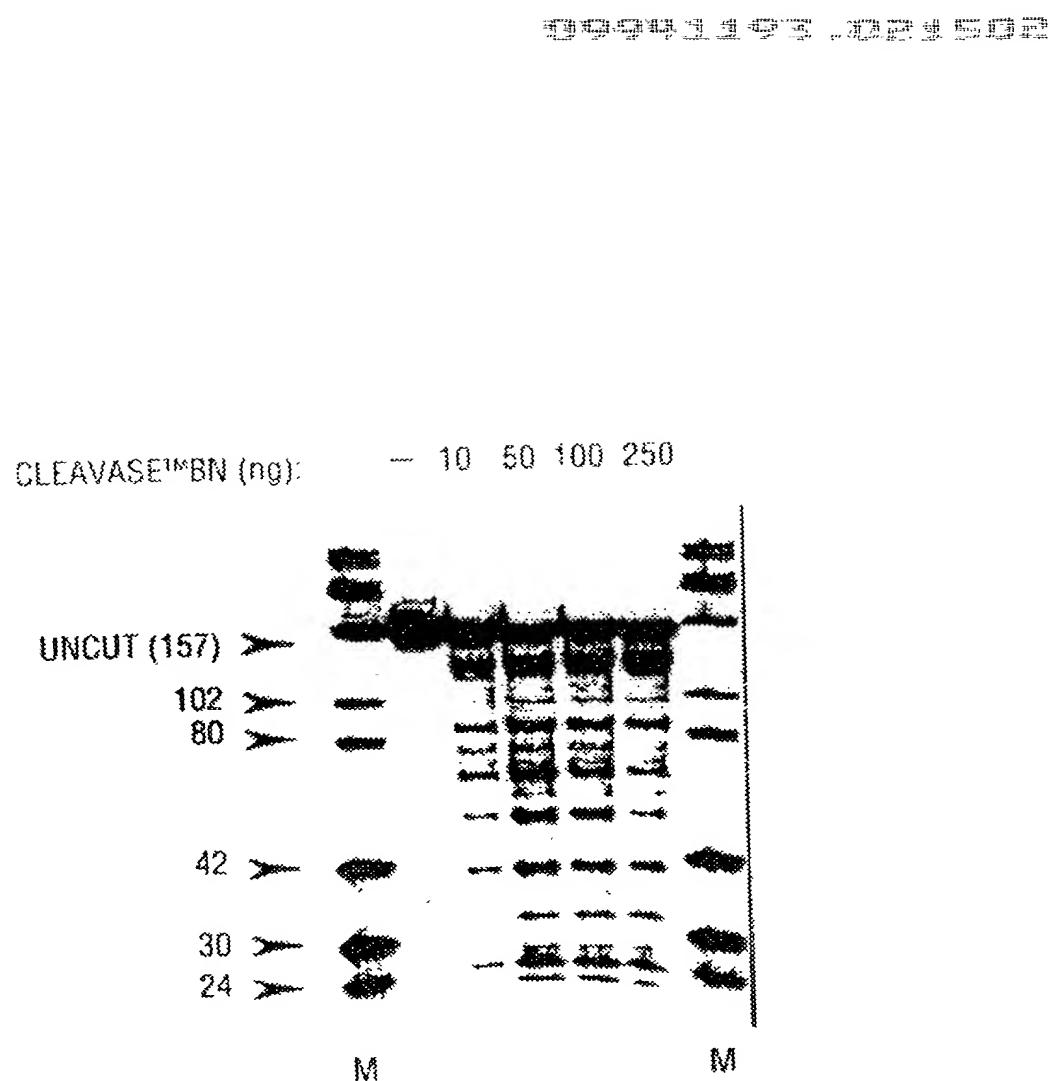


FIG. 37



**FIG. 38**

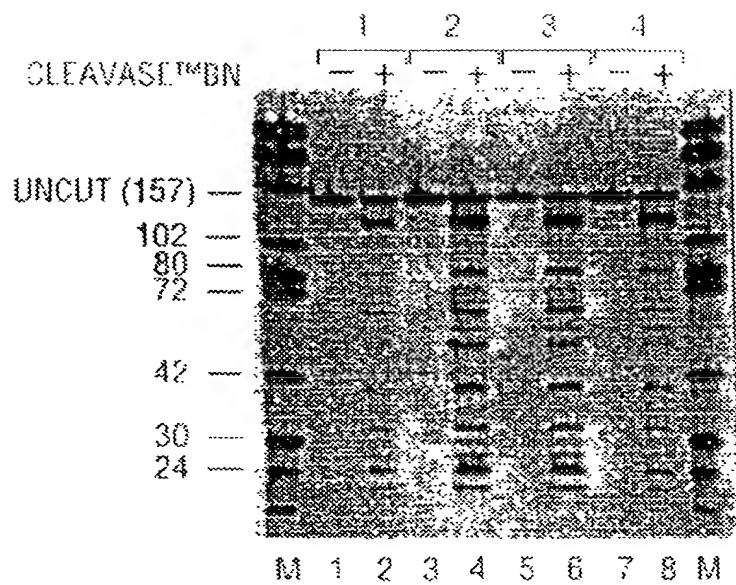


FIG. 39

WT 419 422 419 422 419 422 419 422 419 422

STRAND	5' - BIOTIN SENSE STRAND					5' - FLUORESCIN ANTI-SENSE STRAND						
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ng BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

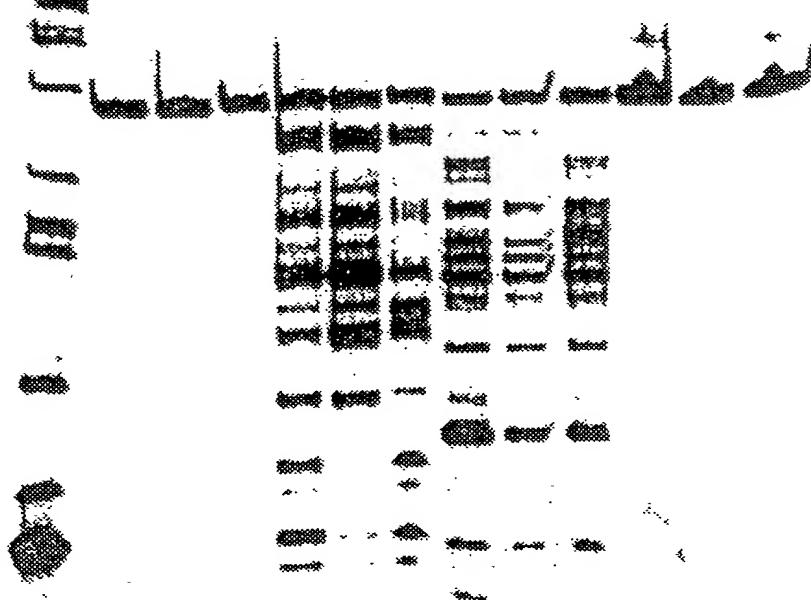


FIG. 40

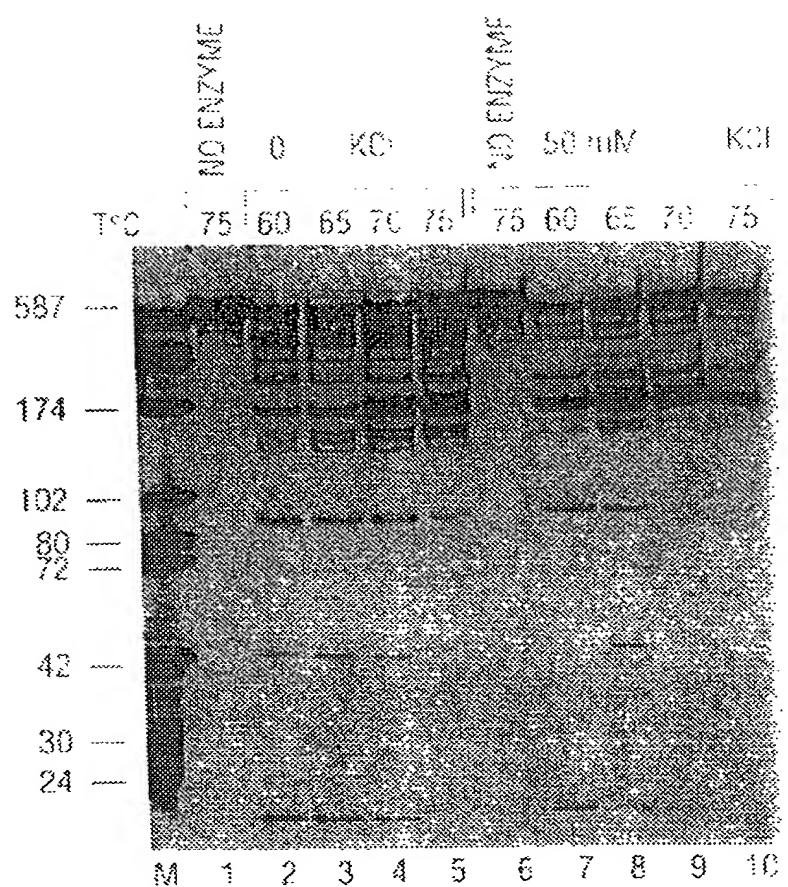
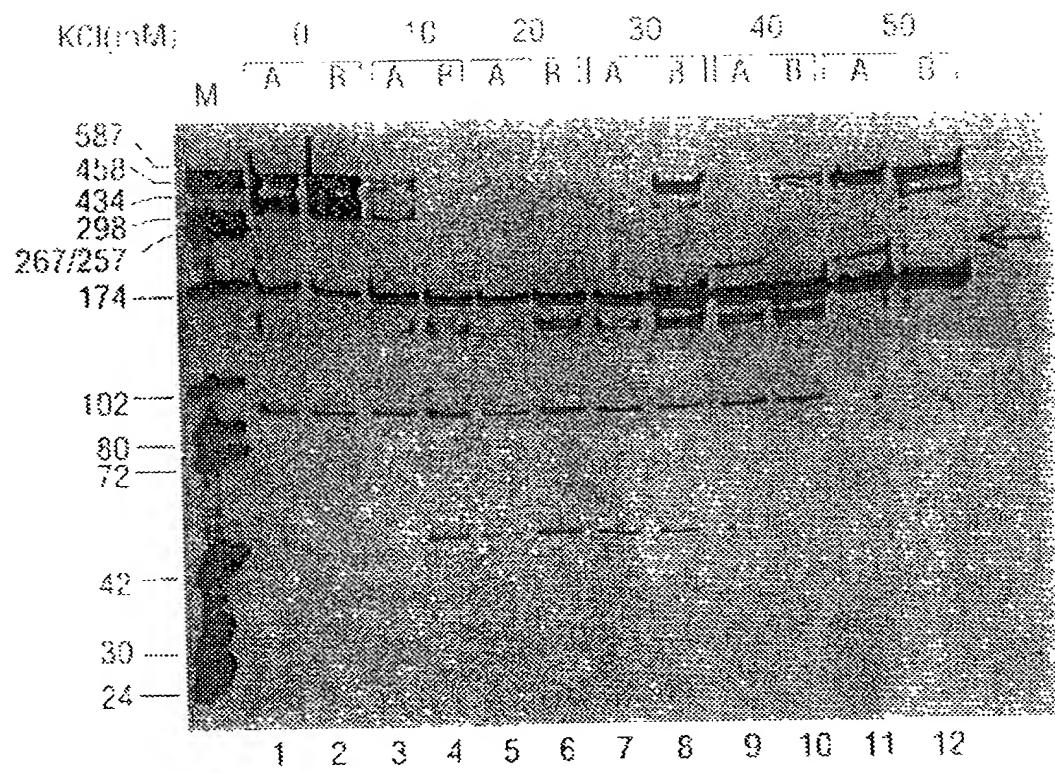


FIG. 41



**FIG. 42**

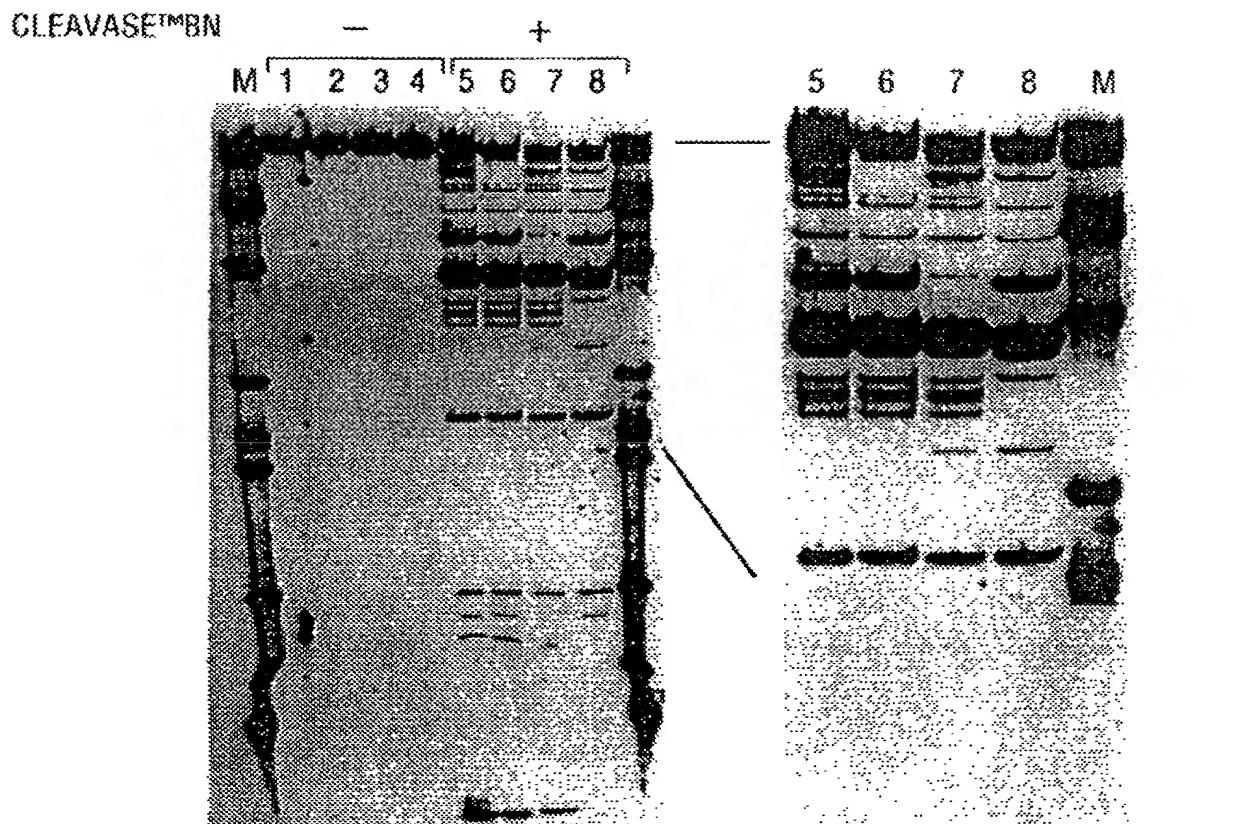


FIG. 43

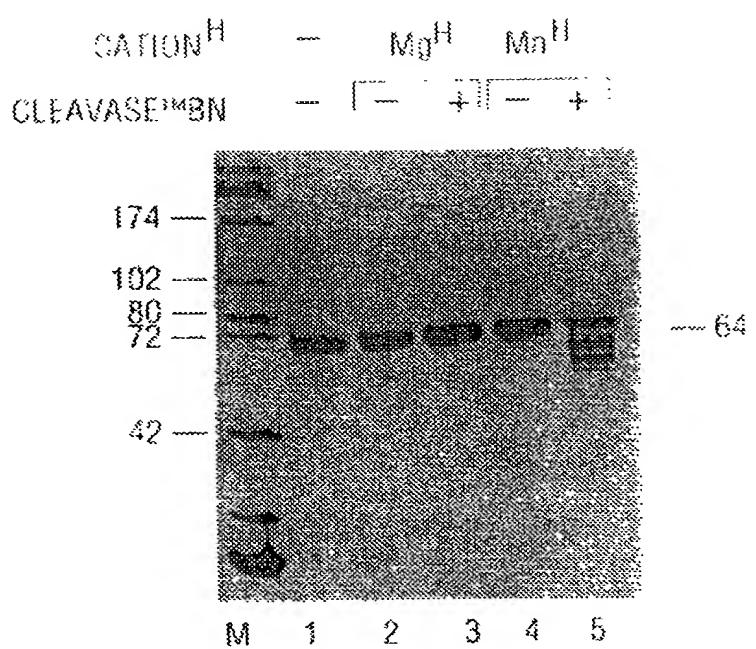


FIG. 44

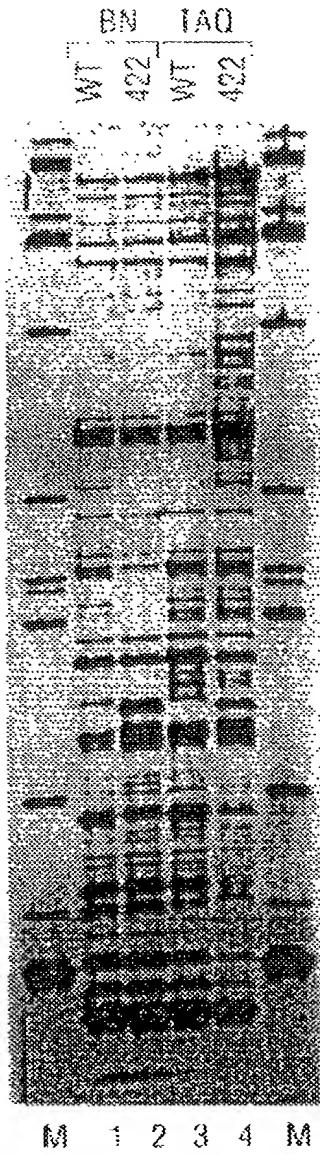
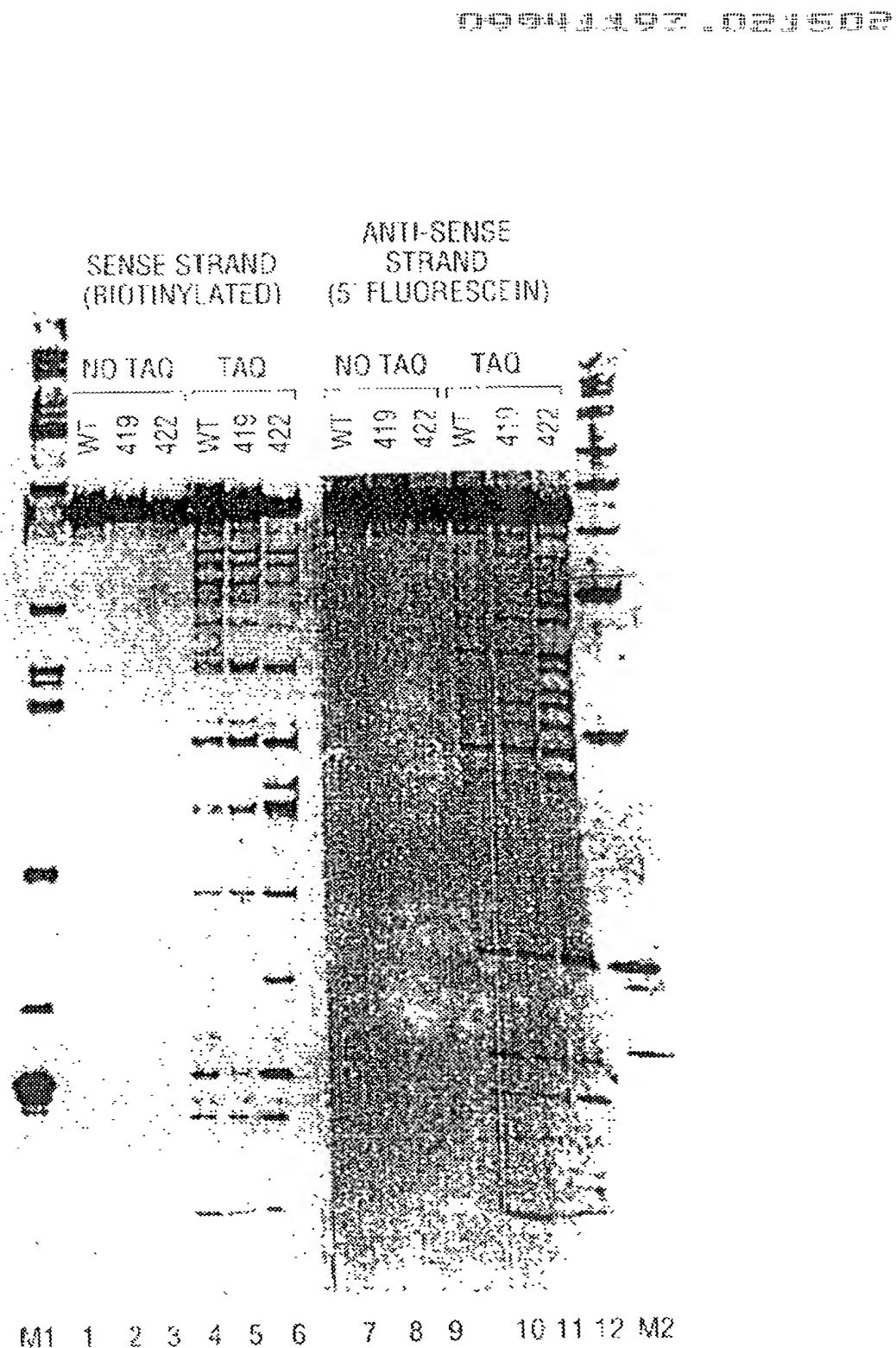
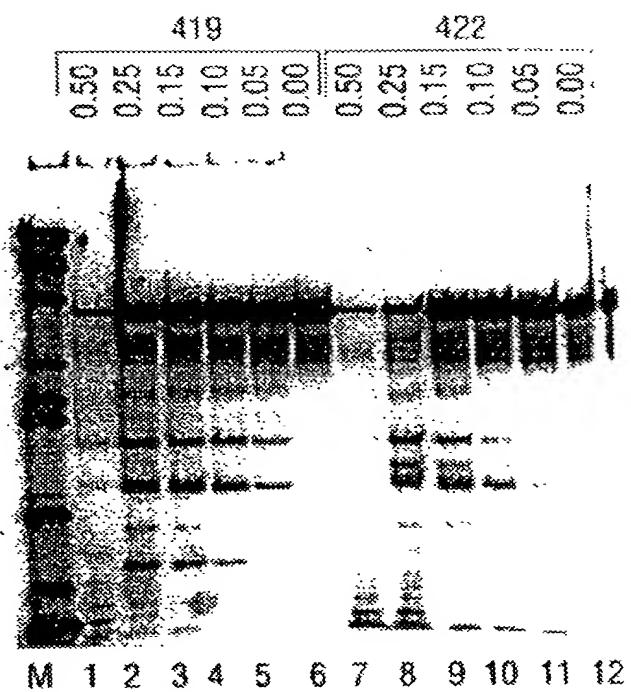


FIG. 45



**FIG. 46**



**FIG. 47**

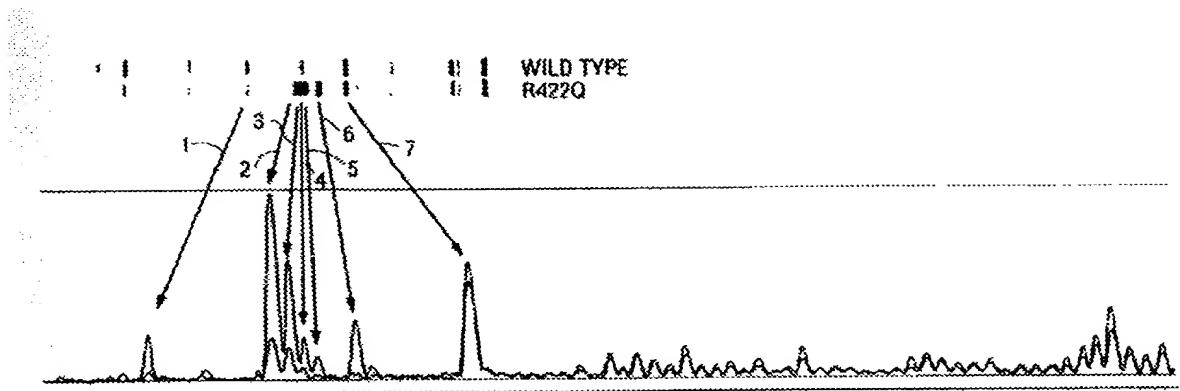


FIG. 48

50  
5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTCTGTCTGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 76)  
  
L.46.16-10 5'GGCTGACAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTCTATCGTCCCTATGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 77)  
  
L.46.16-12 5'GGCTGACAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTCTATCGTCCCTATGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 78)  
  
L19.16-3 5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTCTGTCTGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 79)  
  
L.CEM/251 5'GGCTGACAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTTTGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 80)  
  
L.36.8-3 5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG  
3'CCGACTGTTCTTCCCTTGAGGACTCTGTCTGTCGTTGAAGGTGTTCCCC  
(SEQ ID No: 81)

**FIG. 49A**

## **FIG. 49B**

L.100.8-1  
(SEQ ID NO: 76)  
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGGAACGCCCACTCTCT  
TACAATGCCCTCATGACCCCTCCTGGCCAGCCCCCTGGGTGAGAGA  
100

L.46.16-10  
(SEQ ID NO: 77)  
ATGTTATGGGAGG-----AGCCGGTGGGAACACCCACCTTTCT  
TACAATAACCCCTCC-----TCGGCCAGCCCCCTGGGTGAAAGA

L.46.16-12  
(SEQ ID NO: 78)  
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGGAACGCCCACTTTCTCT  
TACAATGCCCTCATGACCCCTCCTGGCCAGCCCCCTGGGTGAAAGA

L19.16-3  
(SEQ ID NO: 19)  
ATGTTACGGGAGGTACTGGGAAGGAGCCGGTGGGAACGCCCACTTTCT  
TACAATGCCCTCATGACCCCTCCTGGCCAGCCCCCTGGGTGAAAGA

L.CEM/251  
(SEQ ID NO: 80)  
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGGAACGCCCACTCTCT  
TACAATGCCCTCATGACCCCTCCTGGCCAGCCCCCTGGGTGAGAGA

L.36.8-3  
(SEQ ID NO: 81)  
ATGTTACGGGAGGTACTGGGAGGGAGCCGGTGGGAACGCCCACTCTCT  
TACAATGCCCTCATGACCCCTCCTGGCCAGCCCCCTGGGTGAGAGA

L . 100 . 8-1	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACTACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT
L . 46 . 16-10	5' TGGTGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACCACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT
L . 46 . 16-12	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACTACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT
L . 19 . 16-3	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACTACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT
L . CEM / 251	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACTACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT
L . 36 . 8-3	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATT(CAGTCGGCTCTGGGA 3' ACTACATATTATAAGTACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

FIG. 49C

**FIG. 49D**

200  
GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 100 . 8 - 1

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 46 . 16 - 10

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 46 . 16 - 12

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 19 . 16 - 3

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. CEM / 251

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 36 . 8 - 3

GAGGCTGGCAGATTGAGCCCTGGAGGGTTCTCCAGCACCTAGCAGGTAG  
CTCCGACCGGTCAACTCGGACCCCTCAAGAGGGTGTGATCGTCCATC

L. 100. 8 -1      5' AGCCTGGTCCCTGACTCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 76)    3' TCGGACCCACAAGGGACCATCTGAGATGGTCGTGGGACCC

L. 46.16-10      5' AGCCTGGTCCCTGCTAGACTCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 77)    3' TCGGACCCACAAGGGACCATCTGAGATGGTCGTGGGACCC

L. 46.16-12      5' AGCCTGGTCCCTGCTAGACTCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 78)    3' TCGGACCCACAAGGGACCATCTGAGATGGTCGTGGGACCC

L. 19.16-3        5' AGCCTGGTCCCTGCTAGACTCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 79)    3' TCGGACCCACAAGGGACCATCTGAGATGGTCGTGGGACCC

L. CEM/251        5' AGCCTGGTCCCTGCTAGACTCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 80)    3' TCGGACCCACAAGGGACCATCTGAGATGGTCGTGGGACCC

L. 36.8-3        5' AGCCTGAGTGGTCCCTGCTAAACCTCACCAAGGACTCTGAGATGGTCGTGGG  
 (SEQ ID No: 81)    3' TCGGACTCACAAAGGGACGATTGAGATGGTCGTGGGACCC

HAIRPIN

**FIG. 49E**

**FIG. 49F**

300

L. 100; 8 -1  
(SEQ ID NO: 76)

L. 46.16-10  
(SEQ ID NO: 77)

L. 46.16-12  
(SEQ ID NO: 78)

L. 19.16-3  
(SEQ ID NO: 79)

L. CEM/251  
(SEQ ID NO: 80)

L. 36.8-3  
(SEQ ID NO: 81)

CAGAGTGGCTCCACGCCCTTGCTTAAGACCTCTTCATAAAAGCTGCC  
GTCTCAQQGAGGTGGGAACCGAACGAAATTCTGGAGAAGTTATTCGACGG

CAGAGTGGCTCCACGCCCTTGCTTAAGACCTCTTCATAAAAGCTGCC  
GTCTCAQCGAGGTGGGAACCGAACGAAATTCTGGAGAAGTTATTCGACGG

CAGAGTGGCTCCACGCCCTTGCTTAAGACCTCTTCATAAAAGCTGCC  
GTCTCAQCGAGGTGGGAACGAAACGAAATTCTGGAGAAGTTATTCGACGG

CAGAGTGGCTCCACGCCCTTGCTTAAGACCTCTTCATAAAAGCTGCC  
GTCTCAQCGAGGTGGGAACGAAACGAAATTCTGGAGAAGTTATTCGACGG

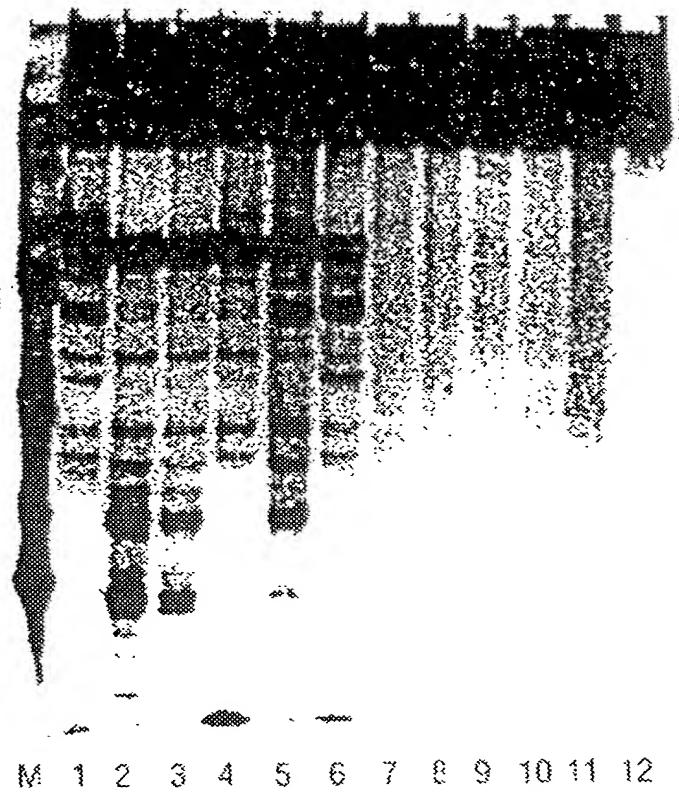
CAGAGTGGACTCCACGCCCTTGCTTAAGACCCCTCTTCATAAAAGCTGCC  
GTCTCAQGTGGTGGGAACGAAACGAAATTCTGGAGAAGTTATTCGACGG

CAGAGCCTCCACGCCCTTGCTTAAGACCTCTTCATAAAAGCTGCC  
GTCTCGDCGAGGTGGGAACGAAACGAAATTCTGGAGAAGTTATTCGACGG

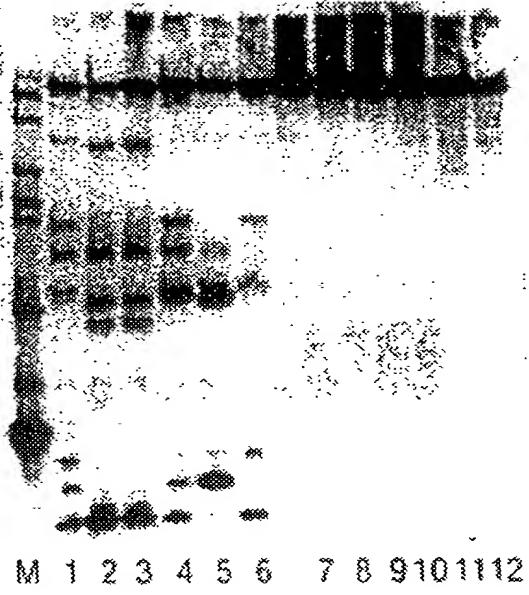
HAIRPIN

L . 100 . 8 - 1	5' ATTTAGAAGTAGGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'
L . 46 , 16 - 10	5' ATTTAGAAGTAAGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'
L . 46 . 16 - 12	5' ATTTAGAAGTAGGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'
L . 19 . 16 - 3	5' ATTTAGAAGTAGGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'
L . CEM / 251	5' ATTTAGAAGTAGGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'
L . 36 . 8 - 3	5' ATTTAGAAGTAGGCCAGTGTGTTCCCATCTCTAGCCCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGGATGGGAC	350 G 3' C 5'

**FIG. 49G**



**FIG. 50**



**FIG. 51**

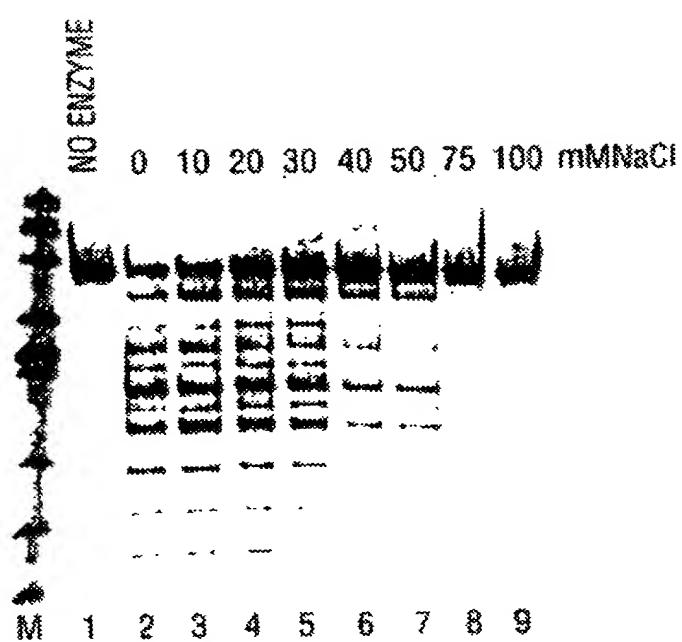


FIG. 52

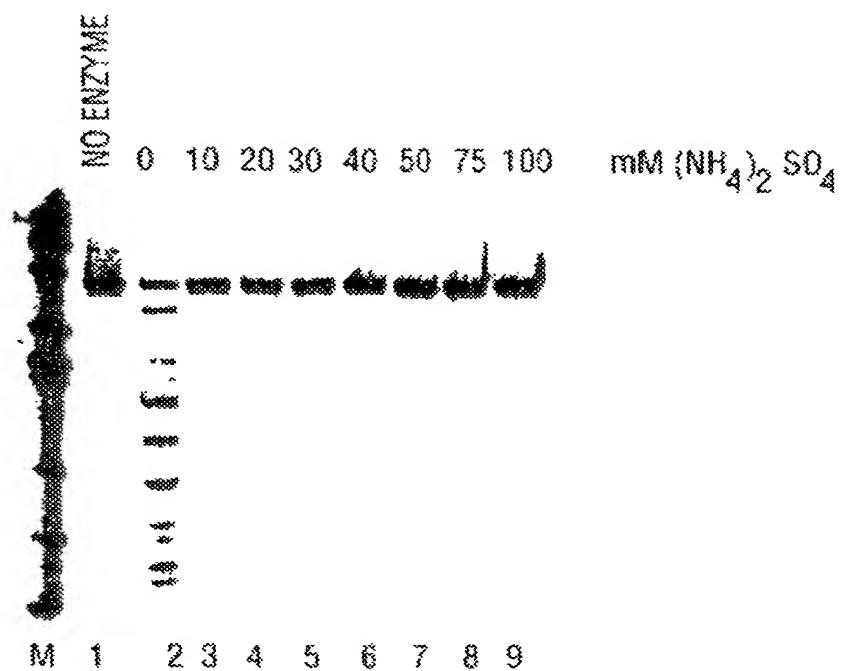
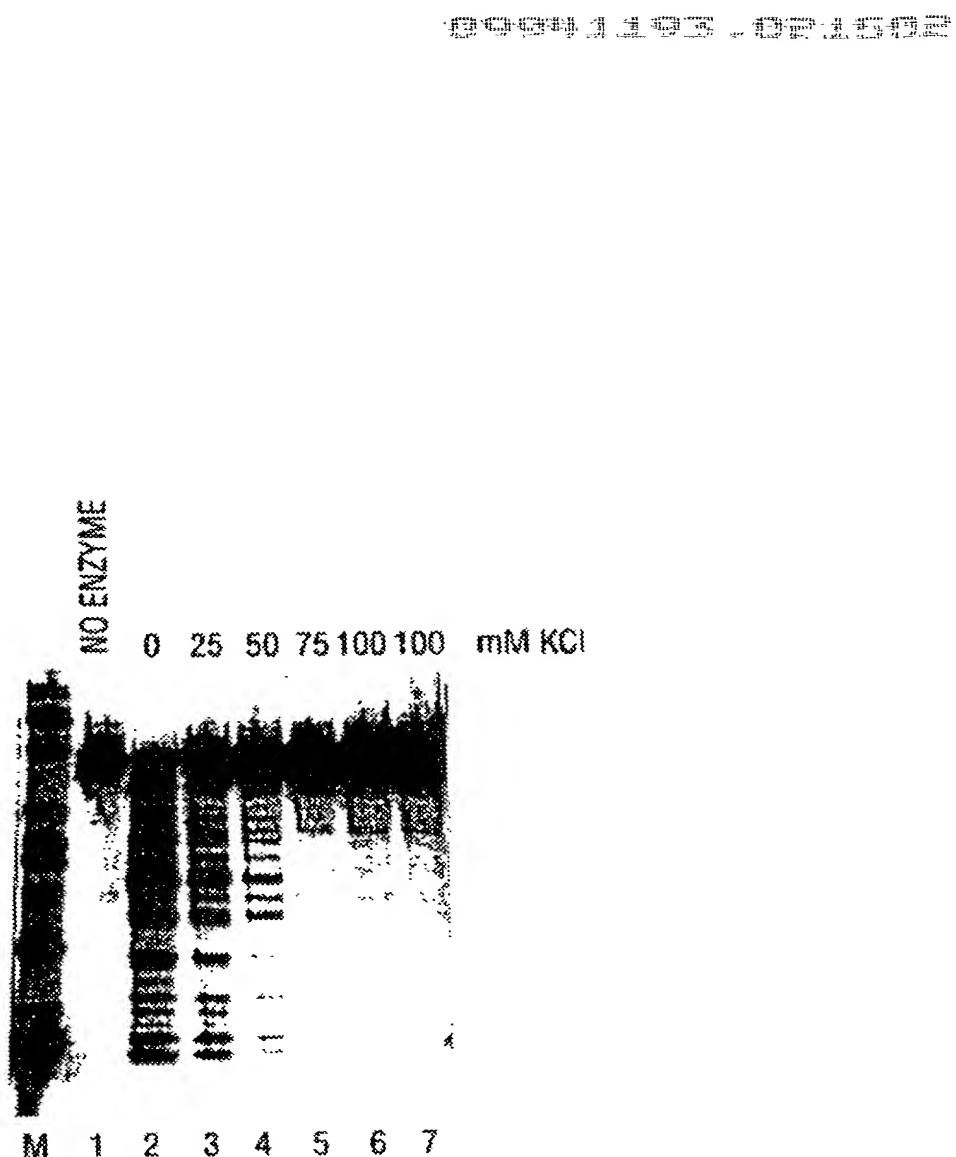
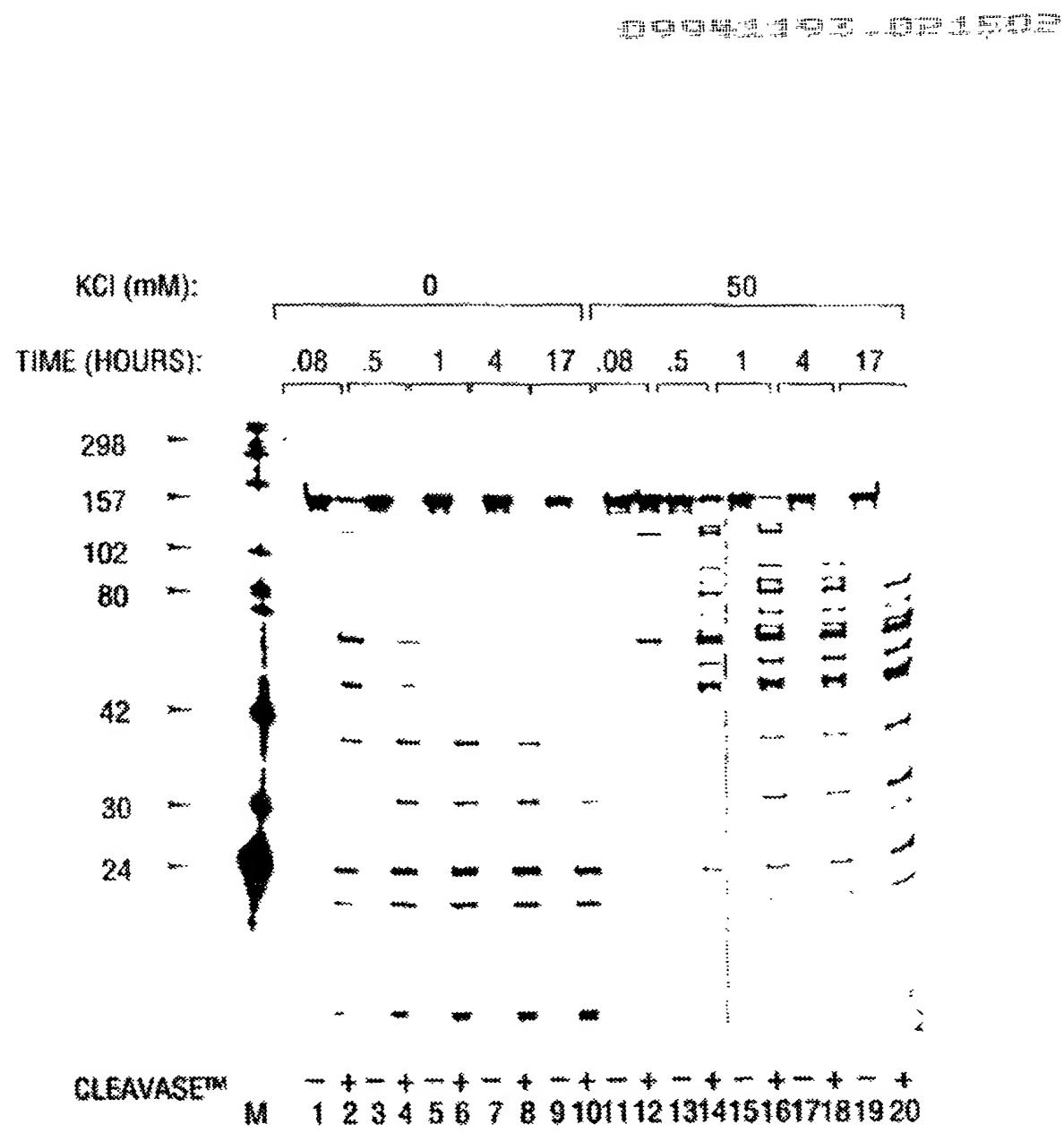


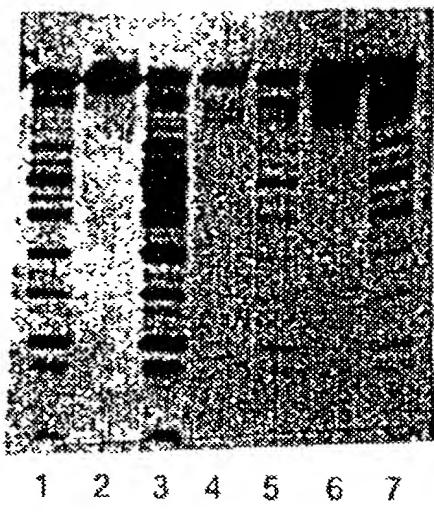
FIG. 53



**FIG. 54**



**FIG. 55**



**FIG. 56**

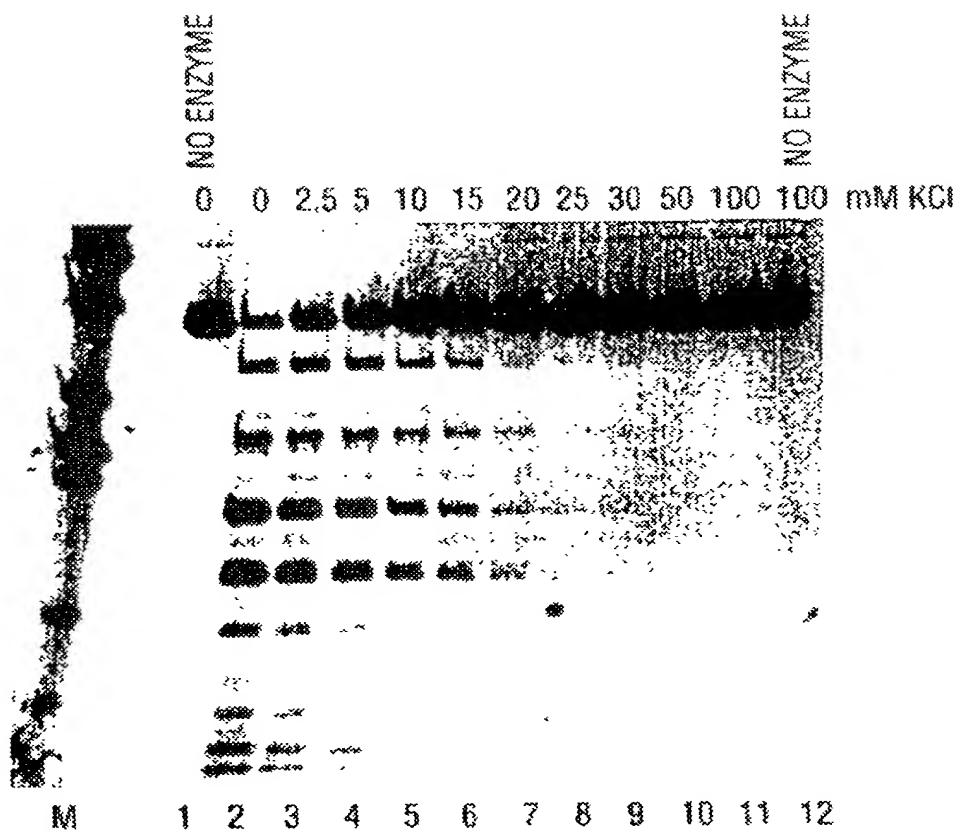


FIG. 57

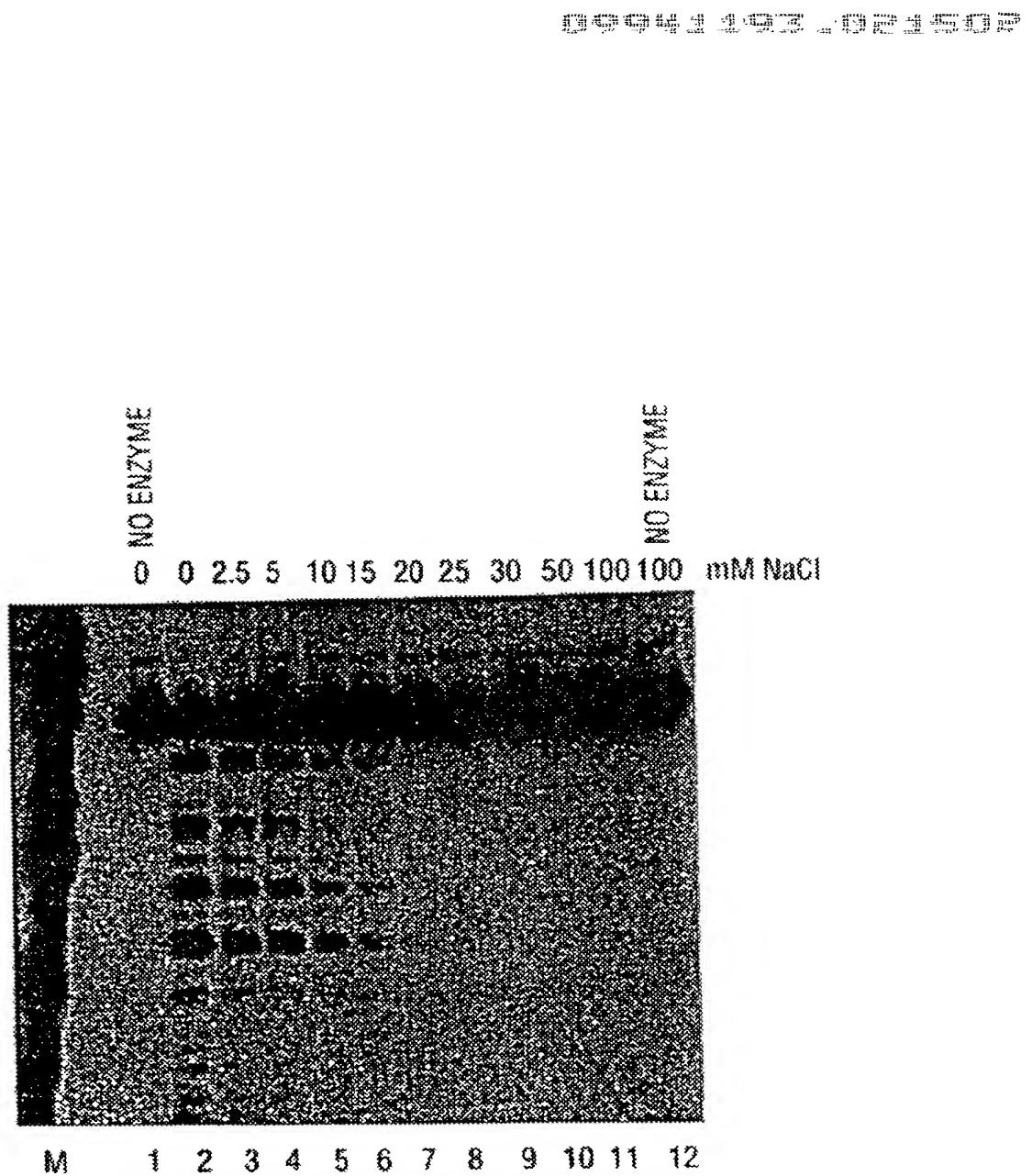


FIG. 58

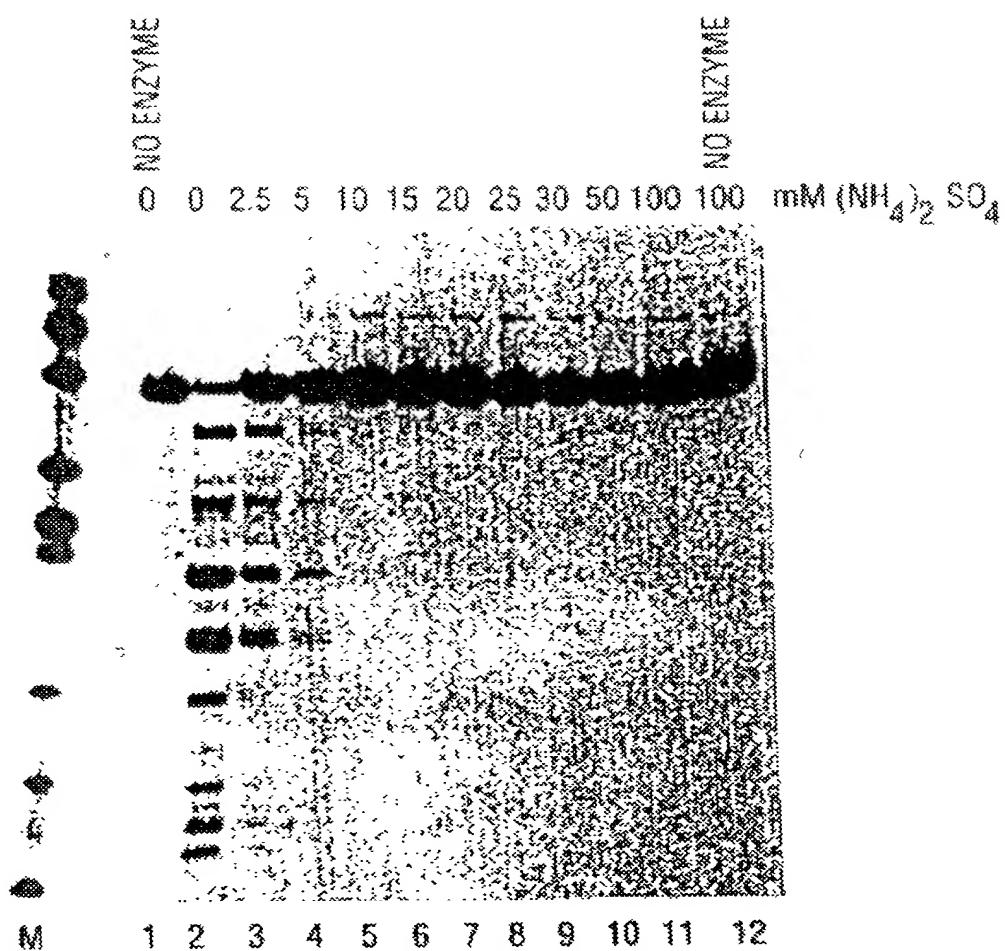
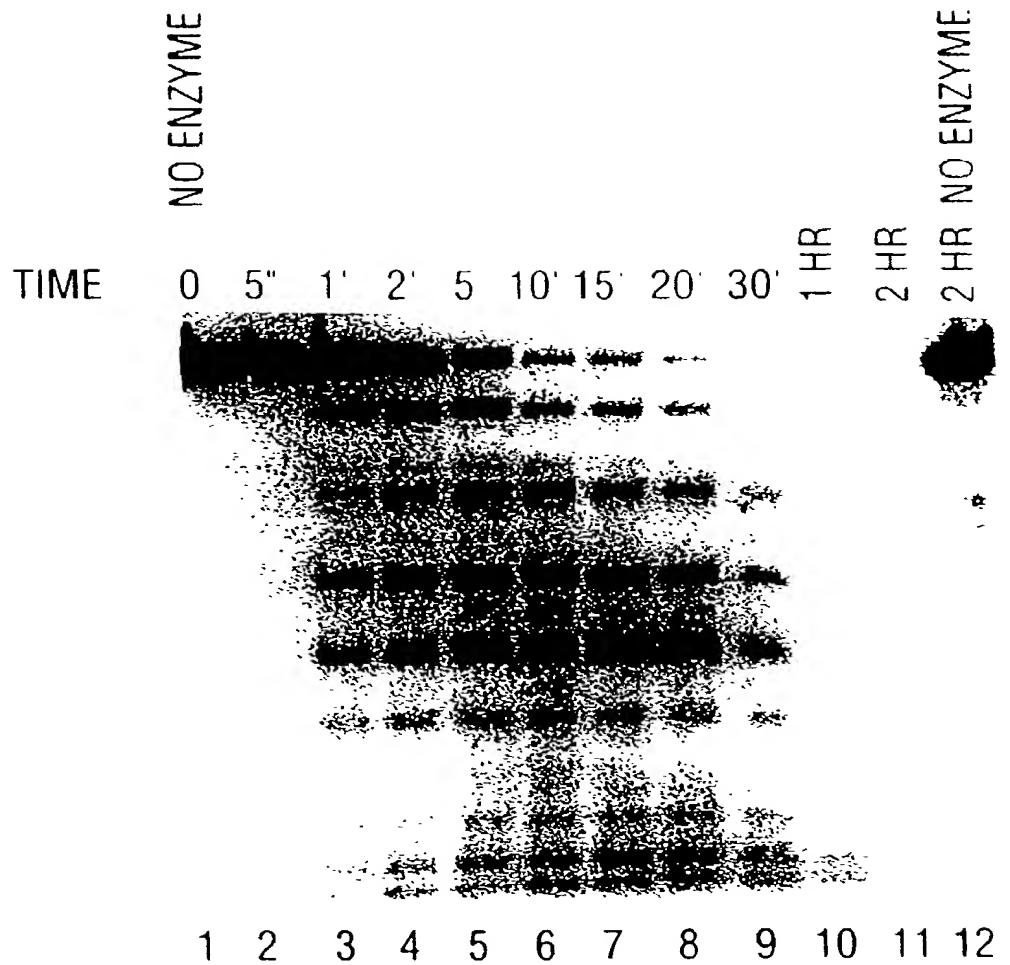


FIG. 59



**FIG. 60**

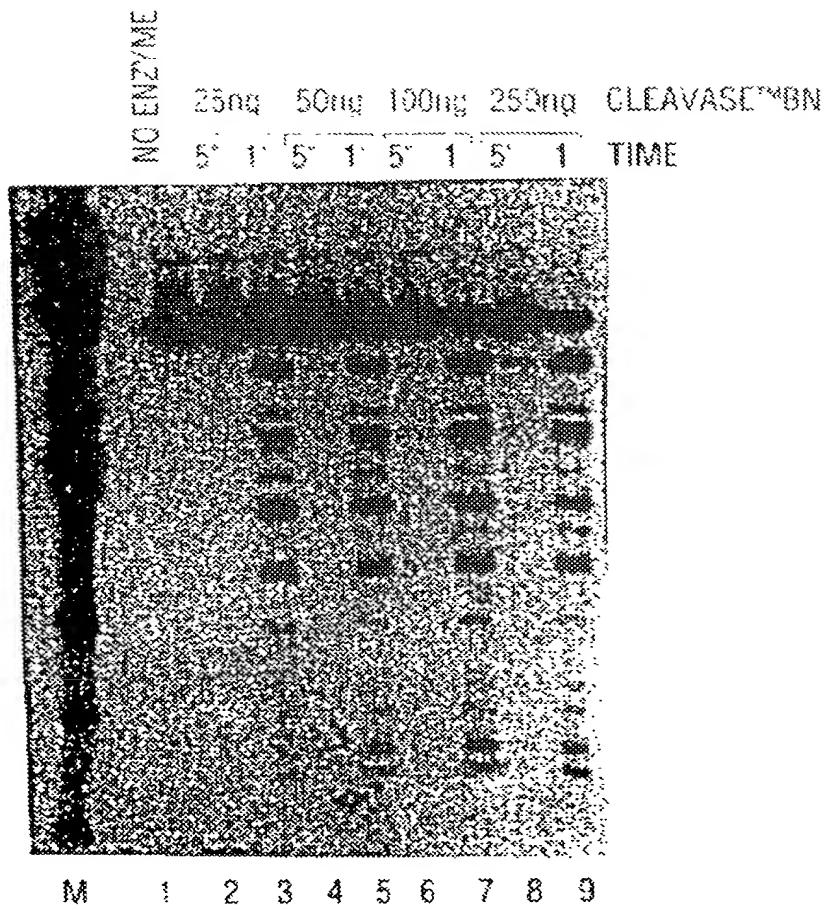


FIG. 61

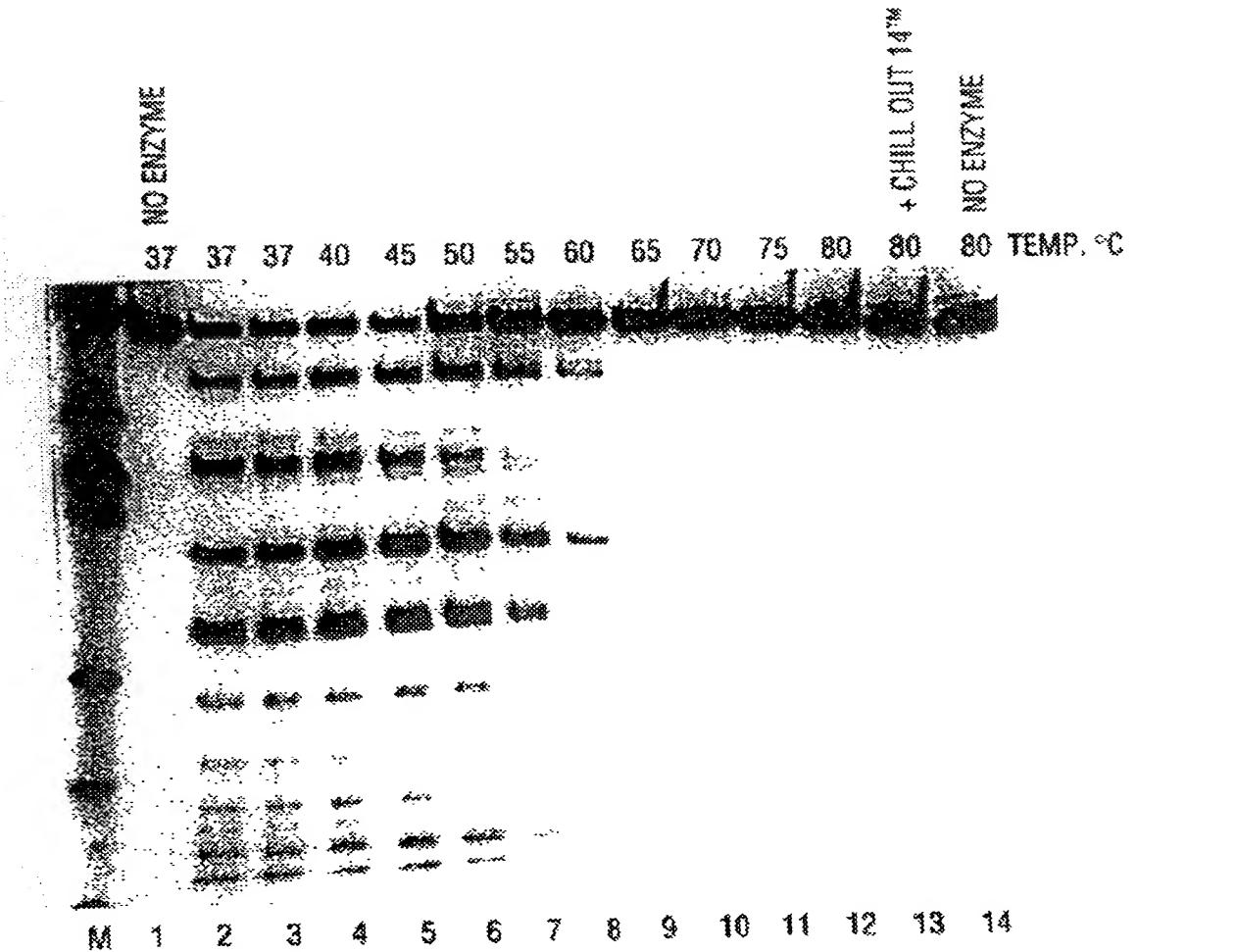


FIG. 62

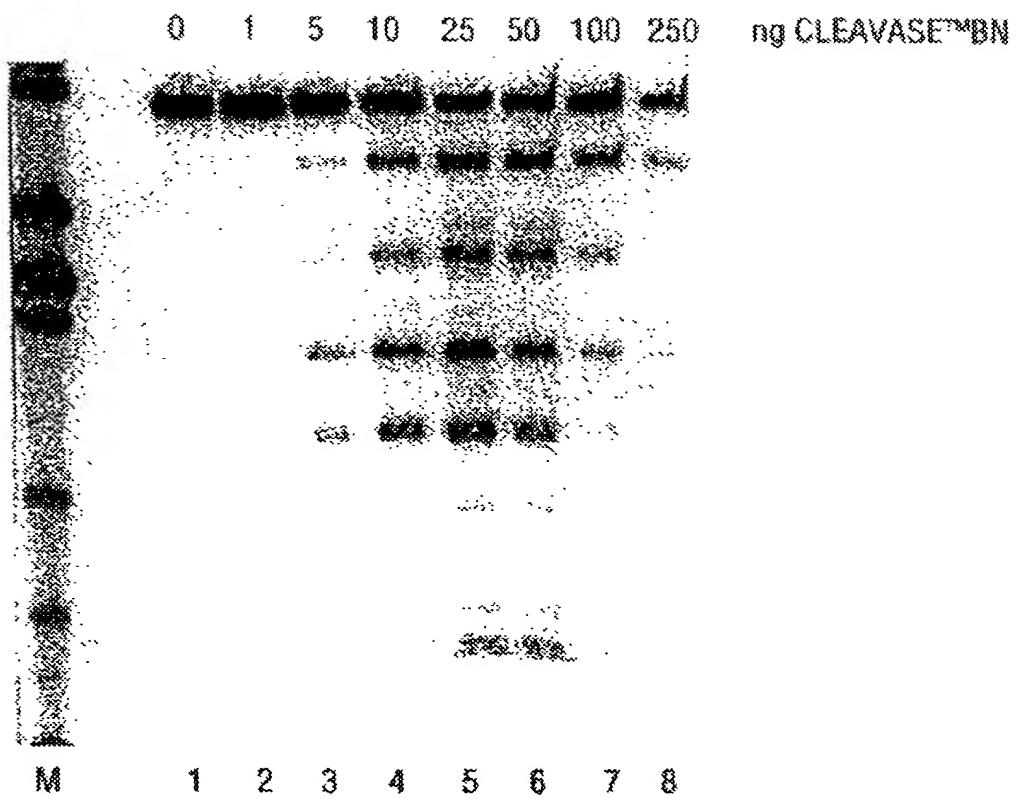


FIG. 63

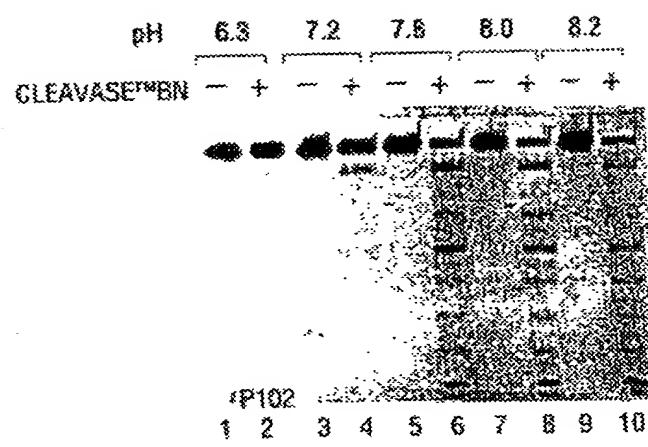


FIG. 64A

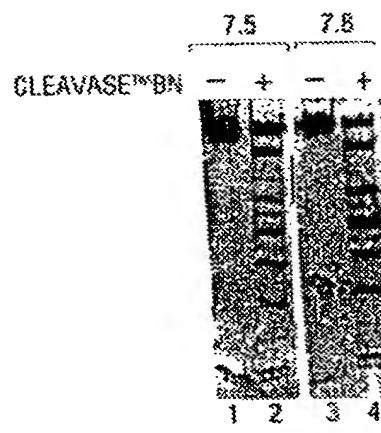
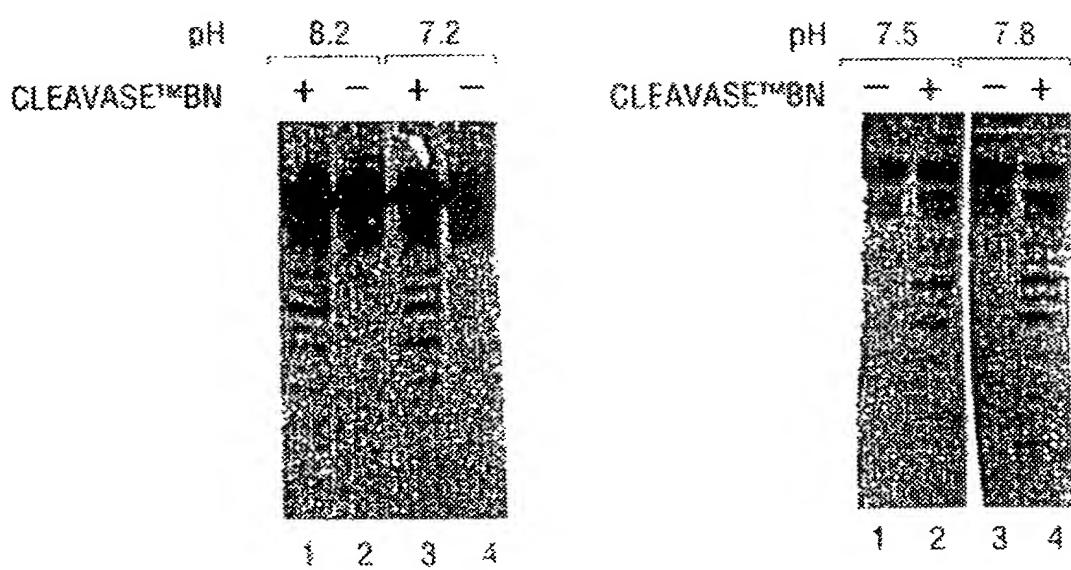


FIG. 64B



**FIG. 65A**

**FIG. 65B**

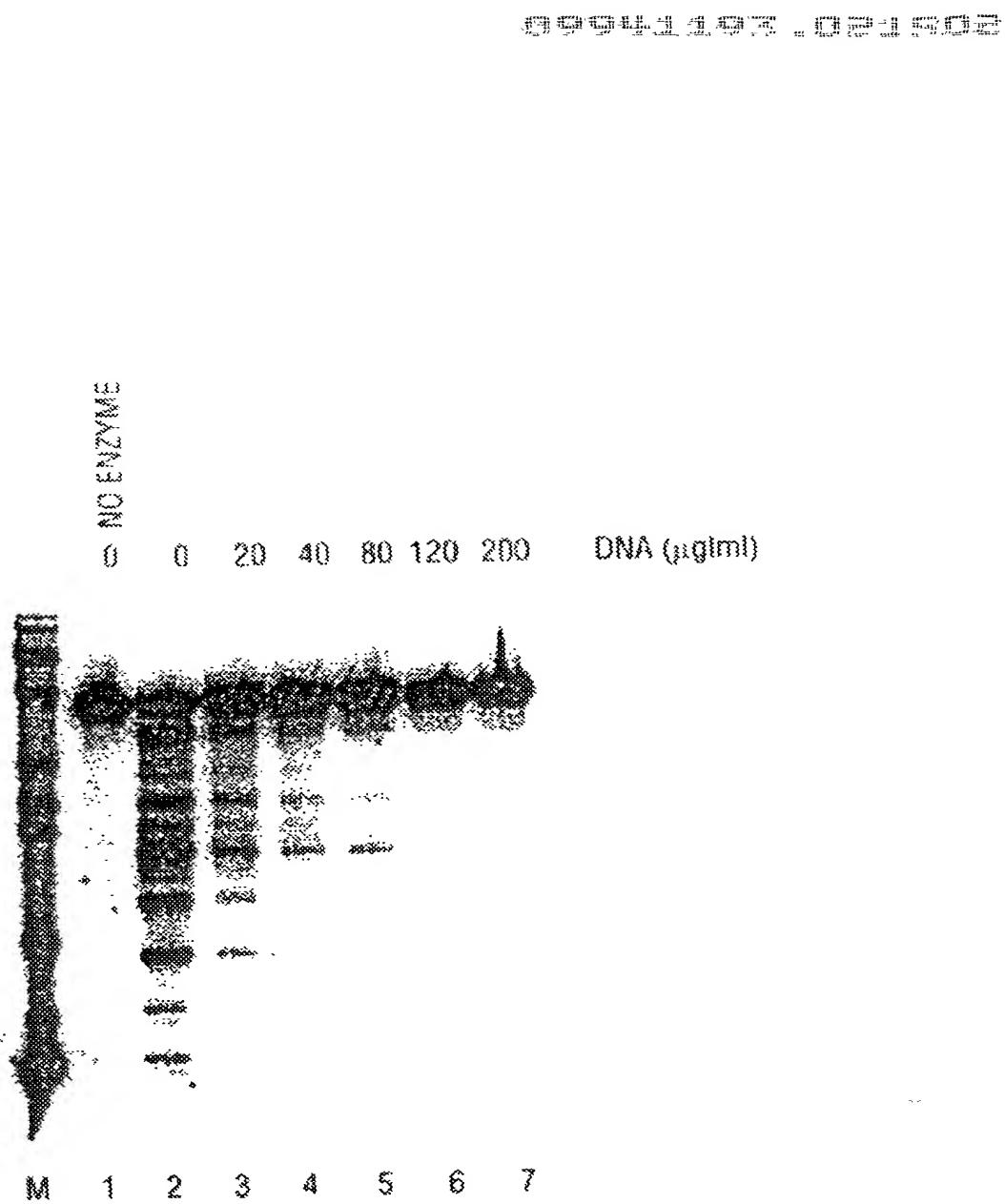
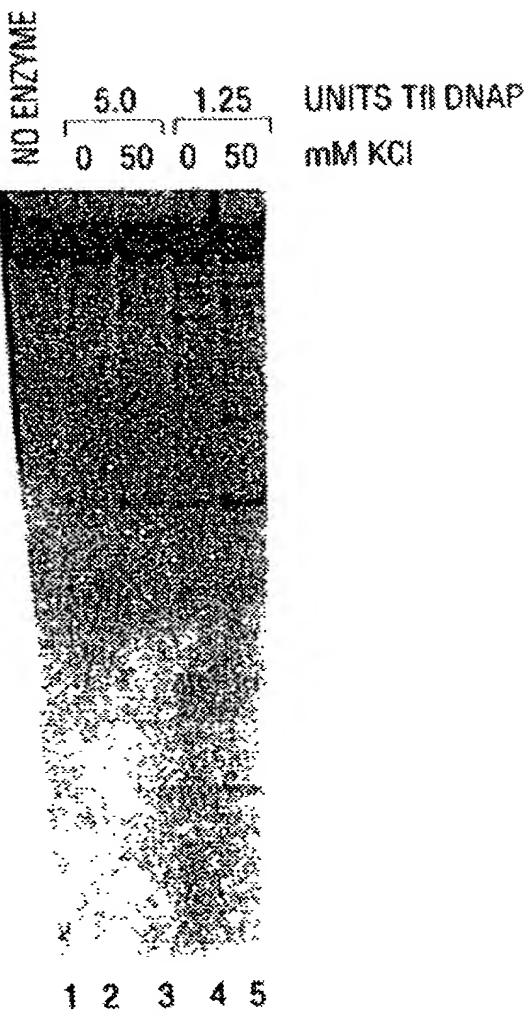


FIG. 66



**FIG. 67**

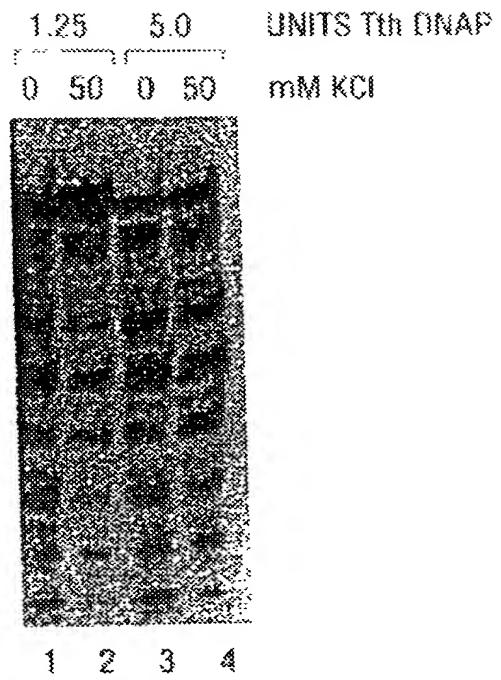


FIG. 68

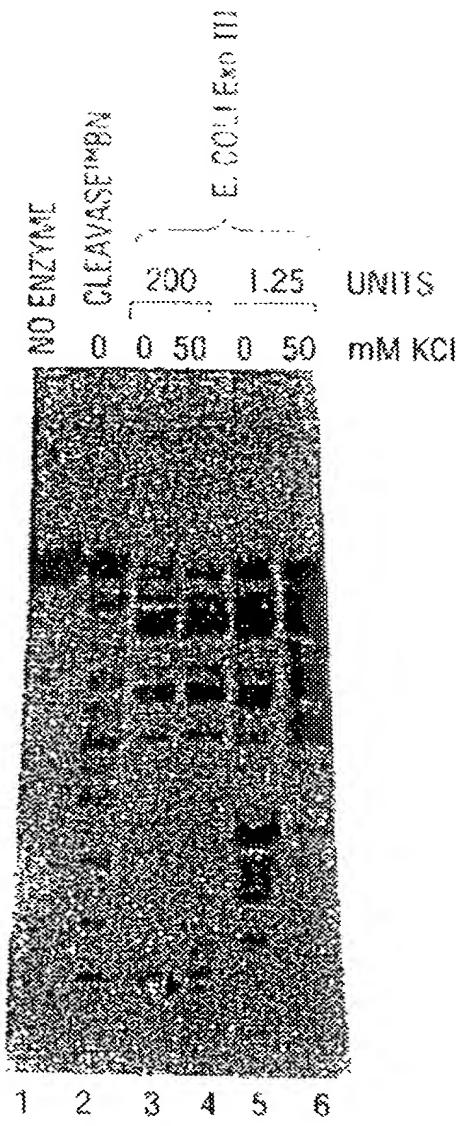
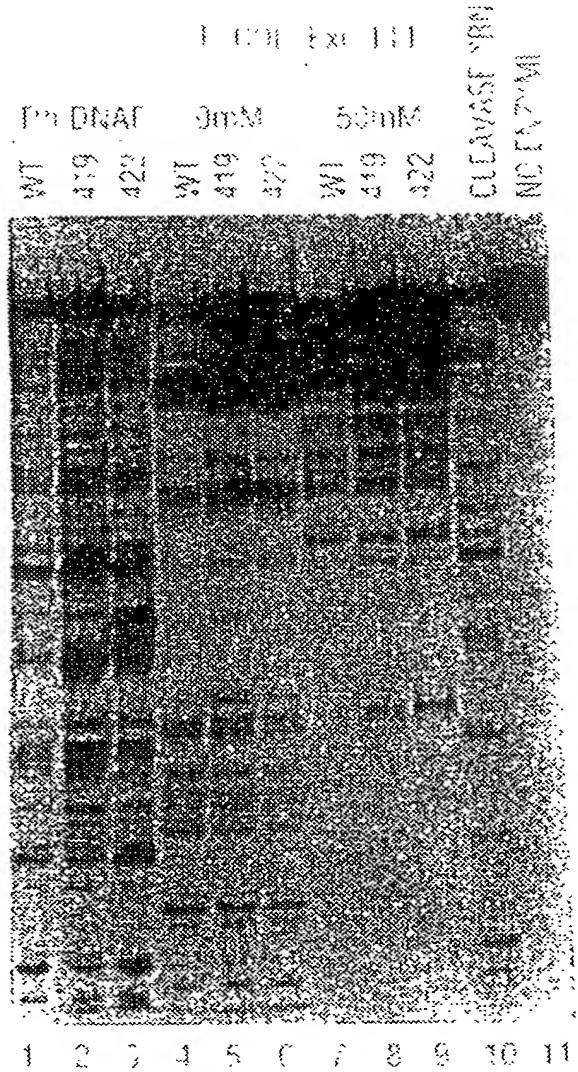
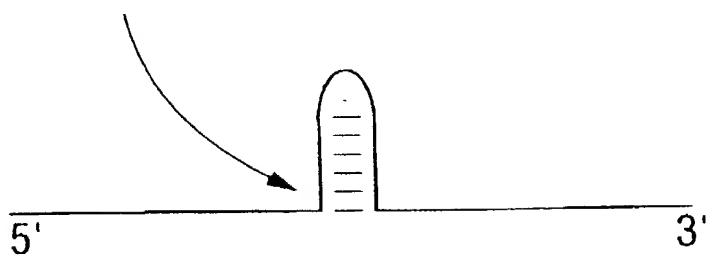


FIG. 69

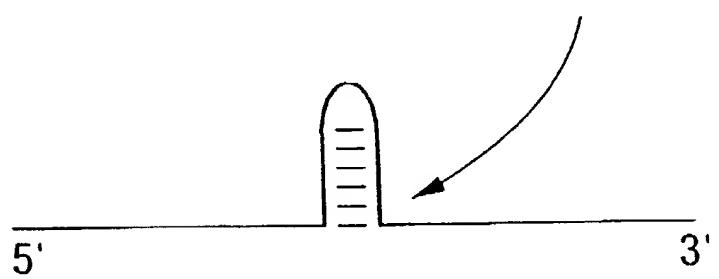


**FIG. 70**

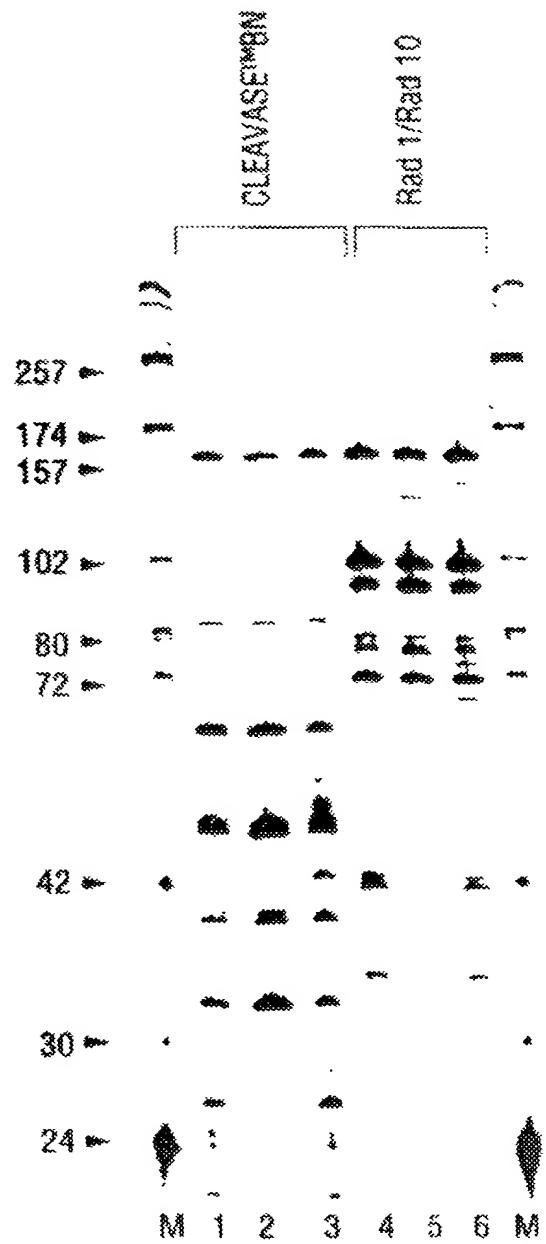
5' CLEAVAGE SITE



3' CLEAVAGE SITE



**FIG. 71**



**FIG. 72**

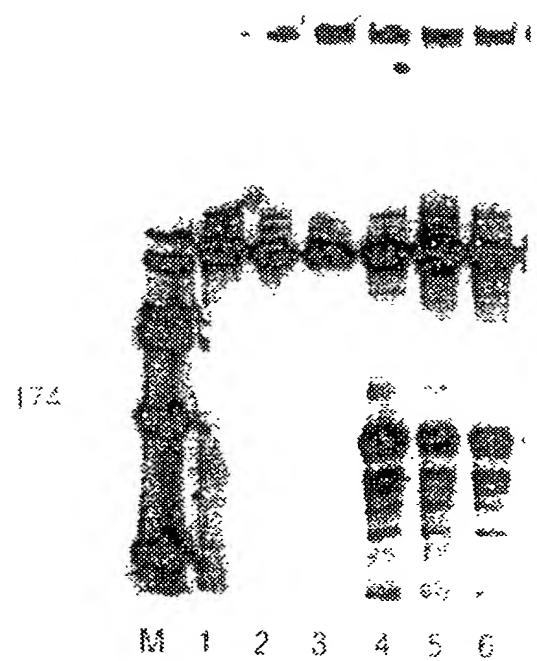
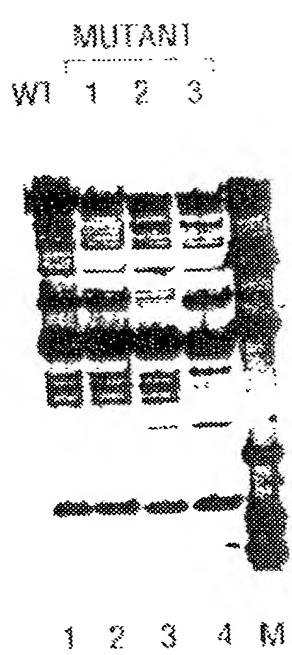
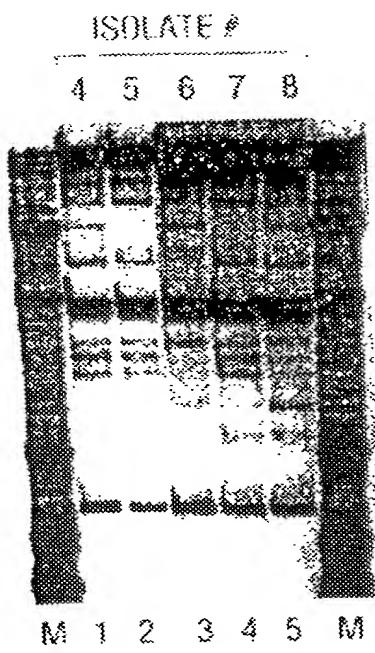


FIG. 73



**FIG. 74A**



**FIG. 74B**

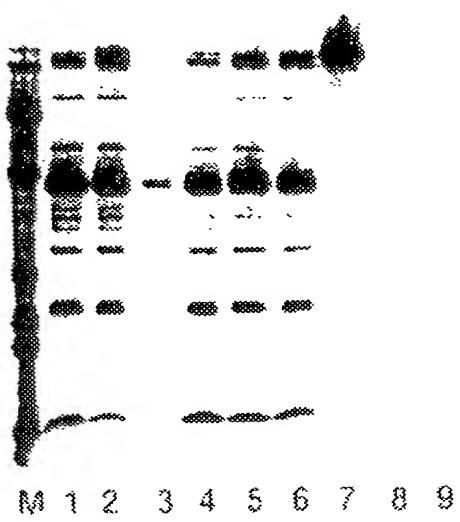
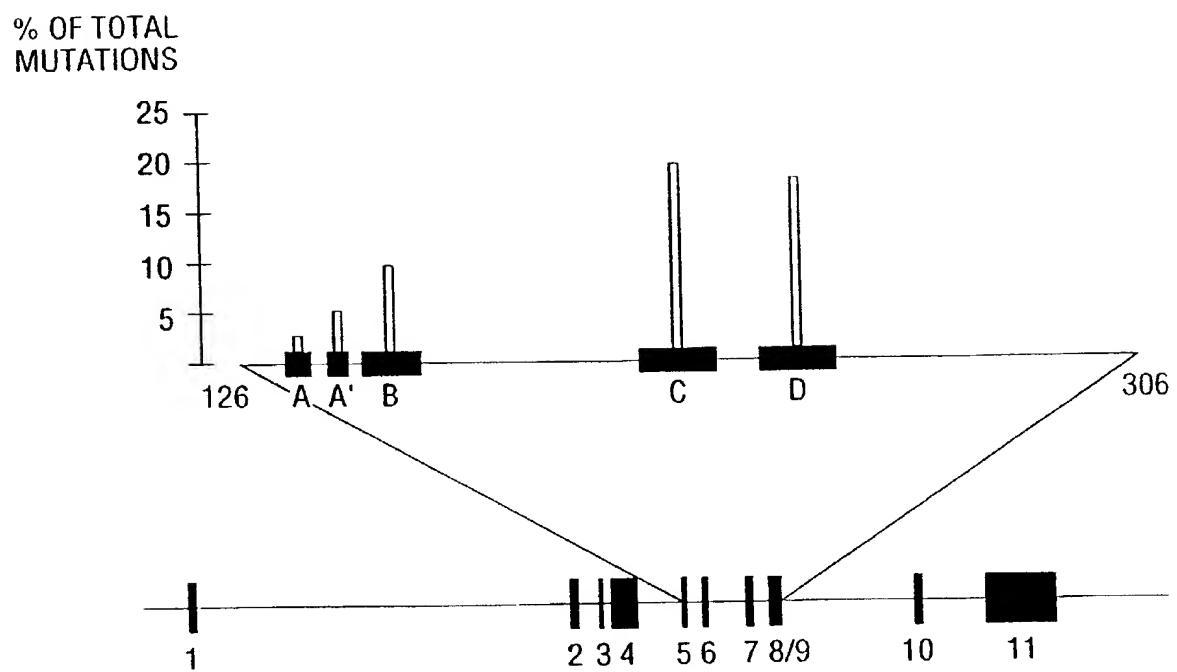
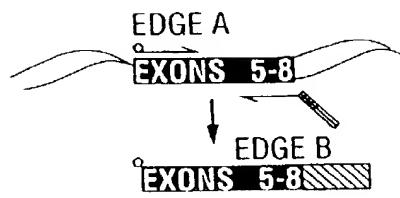


FIG. 75



**FIG. 76**

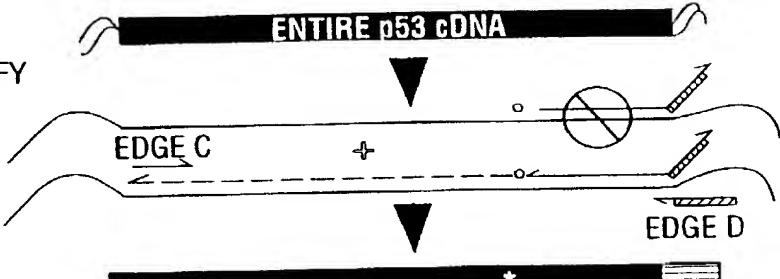
PCR 1  
GENERATE FRAGMENT CONTAINING MUTATION  
ADD AMPLIFIED FRAGMENT TO PCR 2



PCR 2

DENATURE AND AMPLIFY

+ EXONS 5-8



INSERT MUTANT INTO FRAGMENT BY PCR



DIGEST AND CLONE INTO VECTOR



SEQUENCE AND ARCHIVE

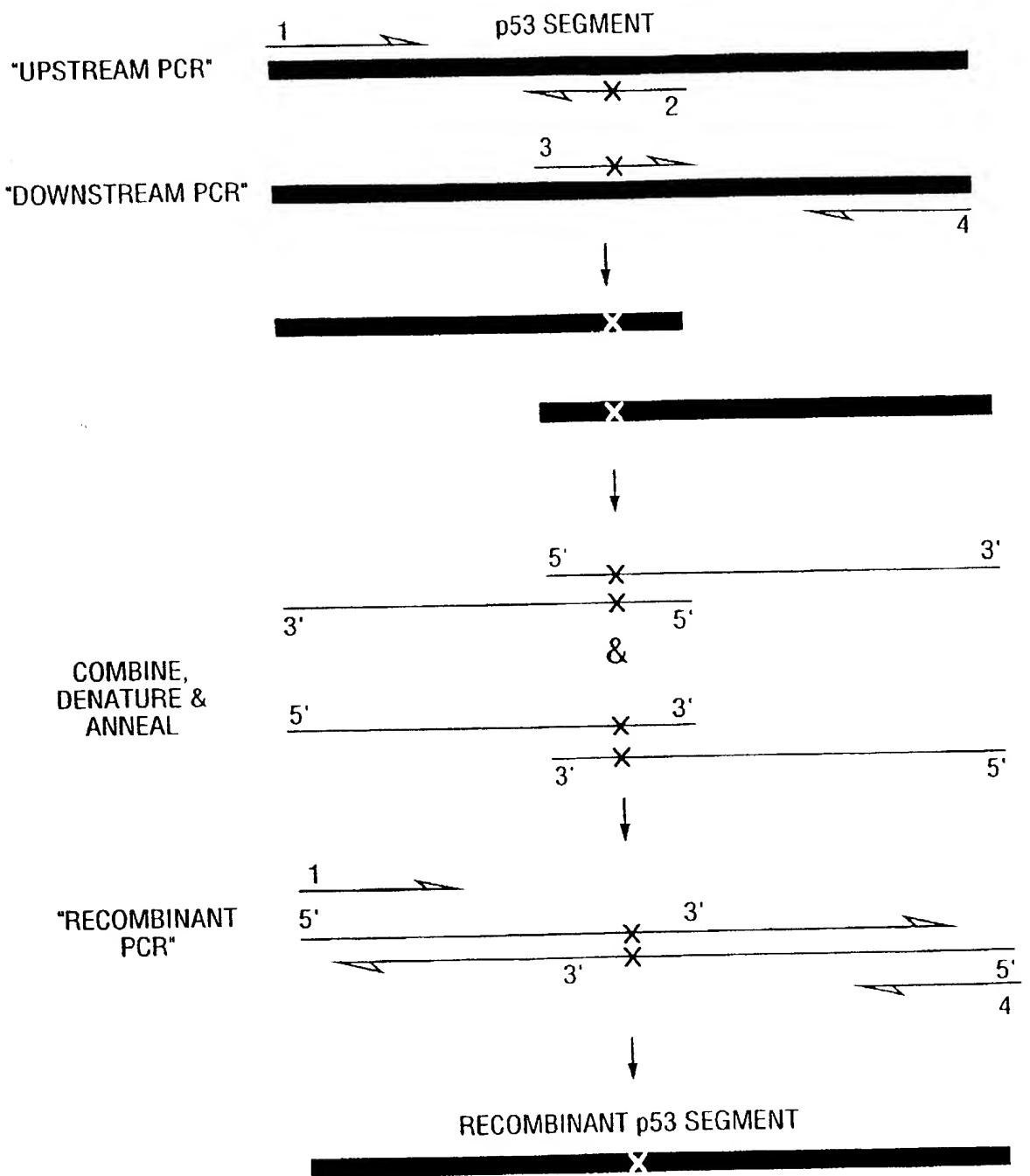


PCR AMPLIFY EXONS 5-8

\* EXONS 5-8



FIG. 77



**FIG. 78**

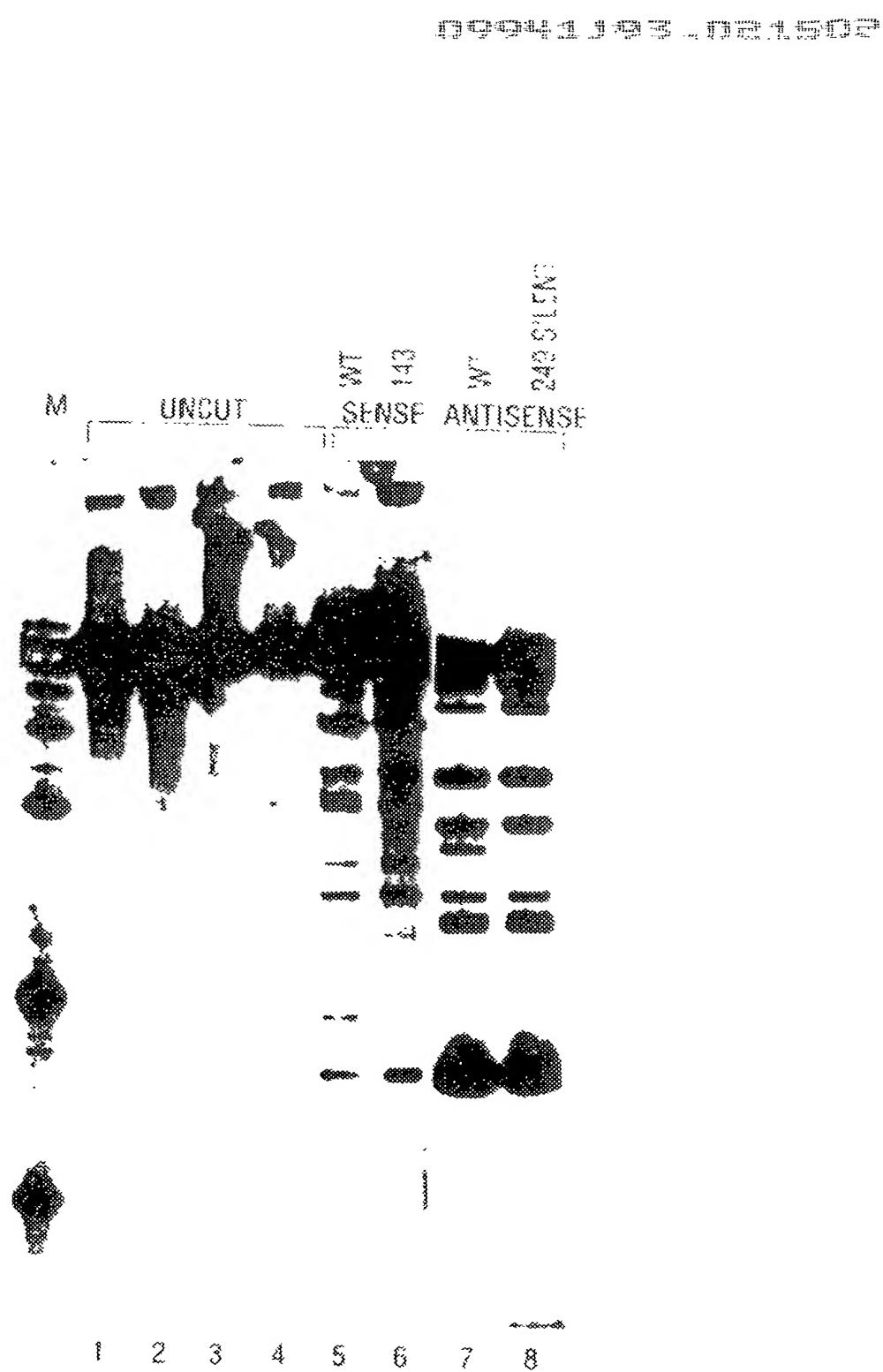
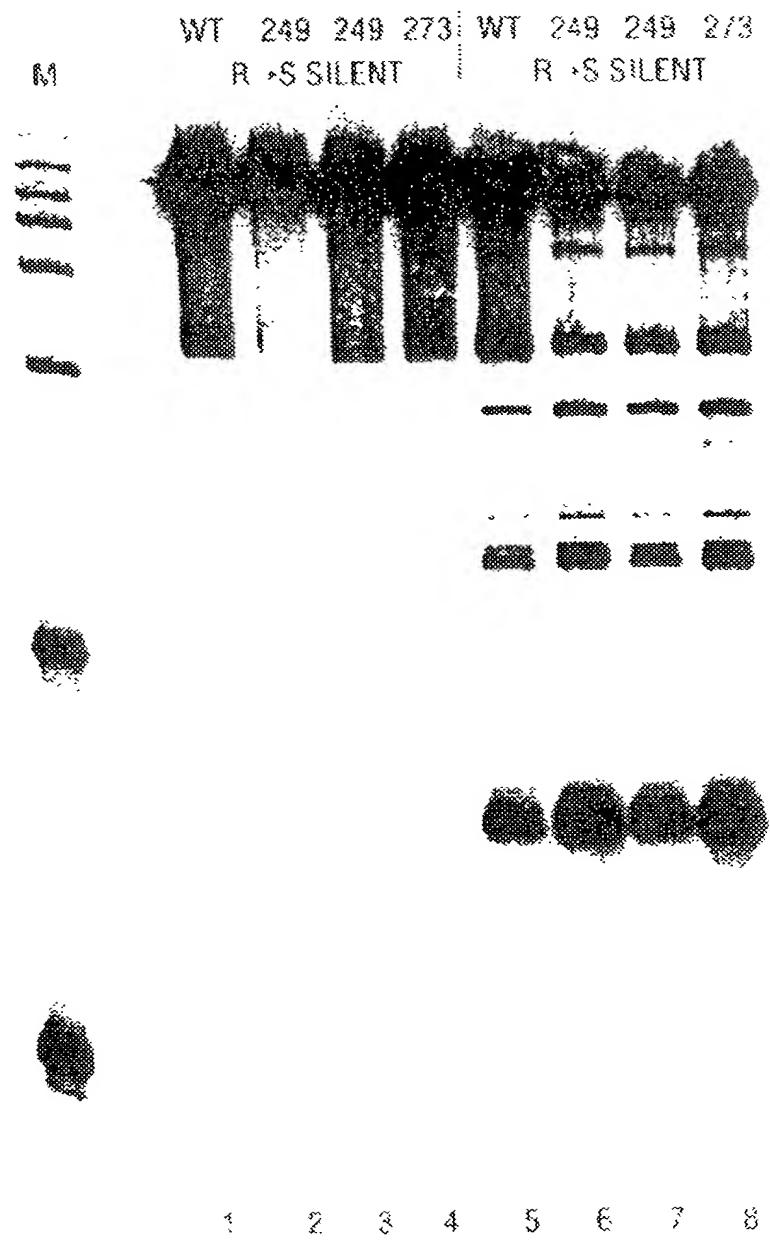
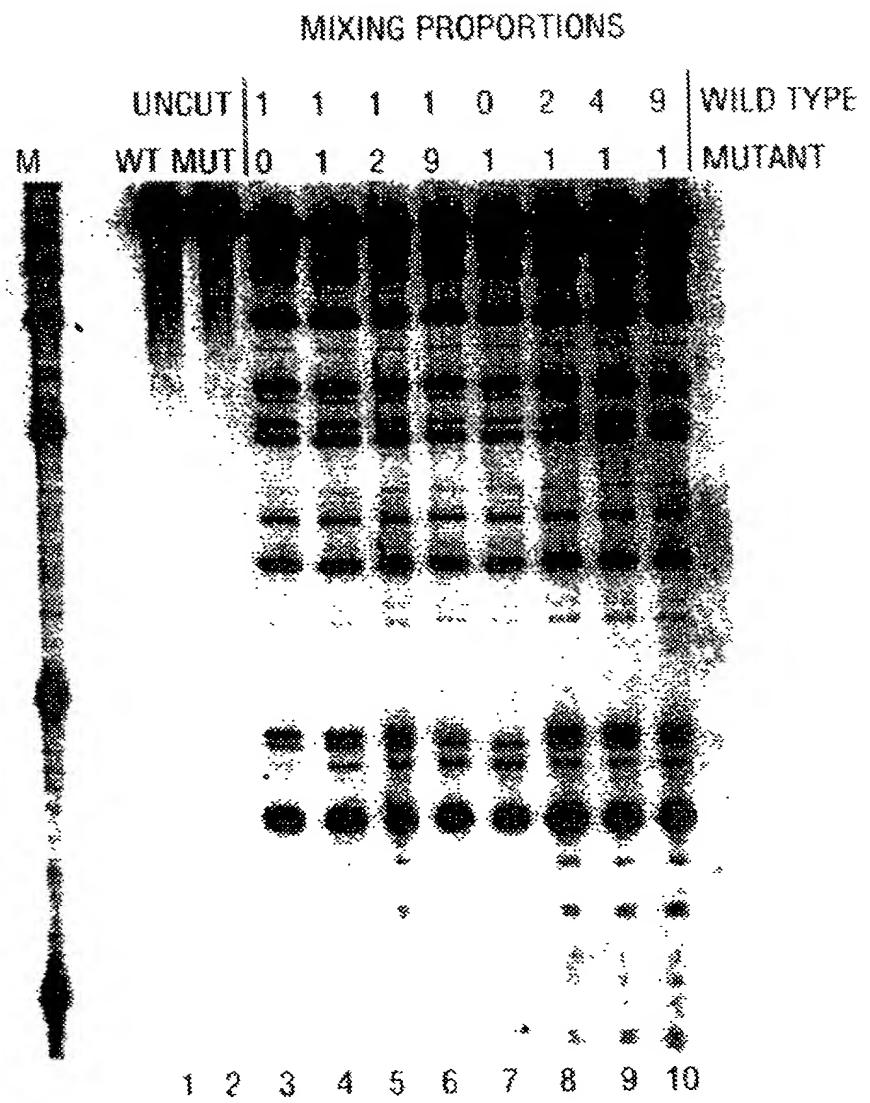


FIG. 79



**FIG. 80**



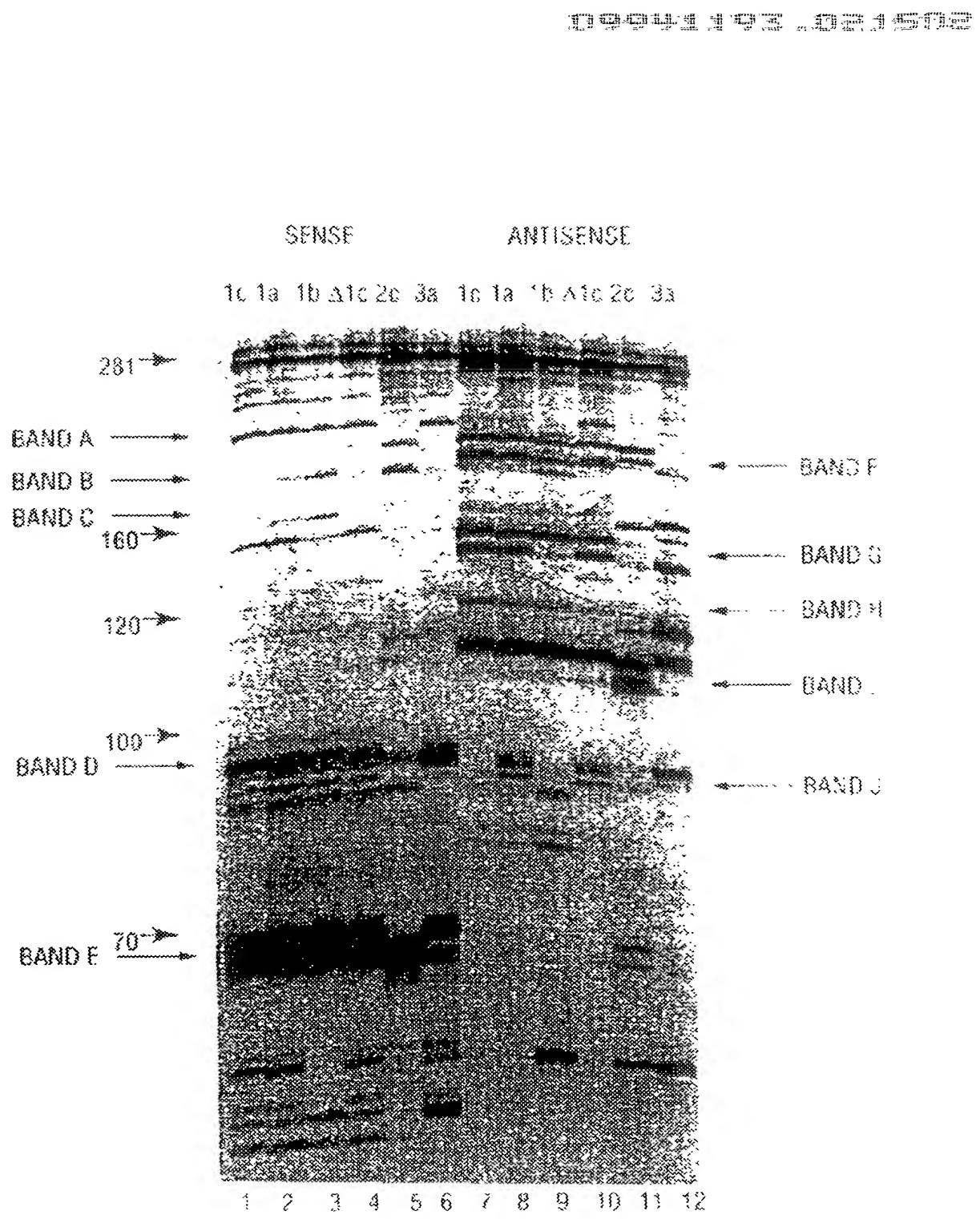
**FIG. 81**

HCV1.1	(SEQ ID NO:121)	1	CTGCTTCAC	CCAGAAAGCG	TCTGGCCATG	GGGTTAGTAT	GAGTGTGCTG	50
HCV2.1	(SEQ ID NO:122)		CTGCTTCAC	CCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTGCTG	
HCV3.1	(SEQ ID NO:123)		CTGCTTCAC	CCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTGCTG	
HCV4.1	(SEQ ID NO:124)		CTGCTTCAC	CCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTGCTG	
HCV4.2	(SEQ ID NO:124)		CTGCTTCAC	CCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTGCTG	
HCV6.1	(SEQ ID NO:125)		CTGCTTCAC	CCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTGCTG	
HCV7.1	(SEQ ID NO:126)		CTGCTTCAC	CCAGAAAGCG	<u>TCTAGCCATG</u>	<u>GGGTTAGTAC</u>	GAGTGTGCTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV3.1			CAGCCTCCAG	<u>GTC</u> CCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV6.1			CAGCCTCCAG	GCCCCCCC	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCCCGGAGAG	CCATAGTGGT	CTGCCGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-AAA	150
HCV2.1			GGTGAGTACA	CCGGAAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAAATTGC	CAGGACGACC	GGGTCCCTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAAATTGC	CAGGACGACC	GGGTCCCTTC	<u>GTGGATGIAA</u>	
HCV6.1			GGTGAGTACA	CCGGAAATTGC	<u>GGGAAGACT</u>	GGGTCCCTTC	TTGGAT-AAA	
HCV7.1			GGTGAGTACA	CCGGAAATTGC	<u>TGGGGTAGCC</u>	GGGTCCCTTC	TTGGAG-CAA	

**FIG. 82A**

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCG <u>G</u> AAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCA <u>CT</u> CAAT	GC <u>CC</u> GGCCAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	<u>AC</u> CC <u>GA</u> AAAT	TTGGGGGTGC	CCCCG <u>G</u> AAGA	T <u>C</u> ACTAGCCG	
HCV1.1	201	AGTAGTGTTC	GGTCCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	250
HCV2.1		AGTAGTGTTC	GGTCCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	
HCV3.1		AGTAGTGTTC	GGTCCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	
HCV4.2		AGTAGTGTTC	GGTCCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	
HCV6.1		AGTAGGTTG	GGT <u>I</u> CCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	
HCV7.1		AGTAGTGTTC	GGTCCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGT <u>G</u> CCT	
HCV1.1	251	GGGAGTGCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GGGAGTCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GGGAGTCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GGGAGTACC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GGGAGTCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1							

**FIG. 82B**



**FIG. 83**

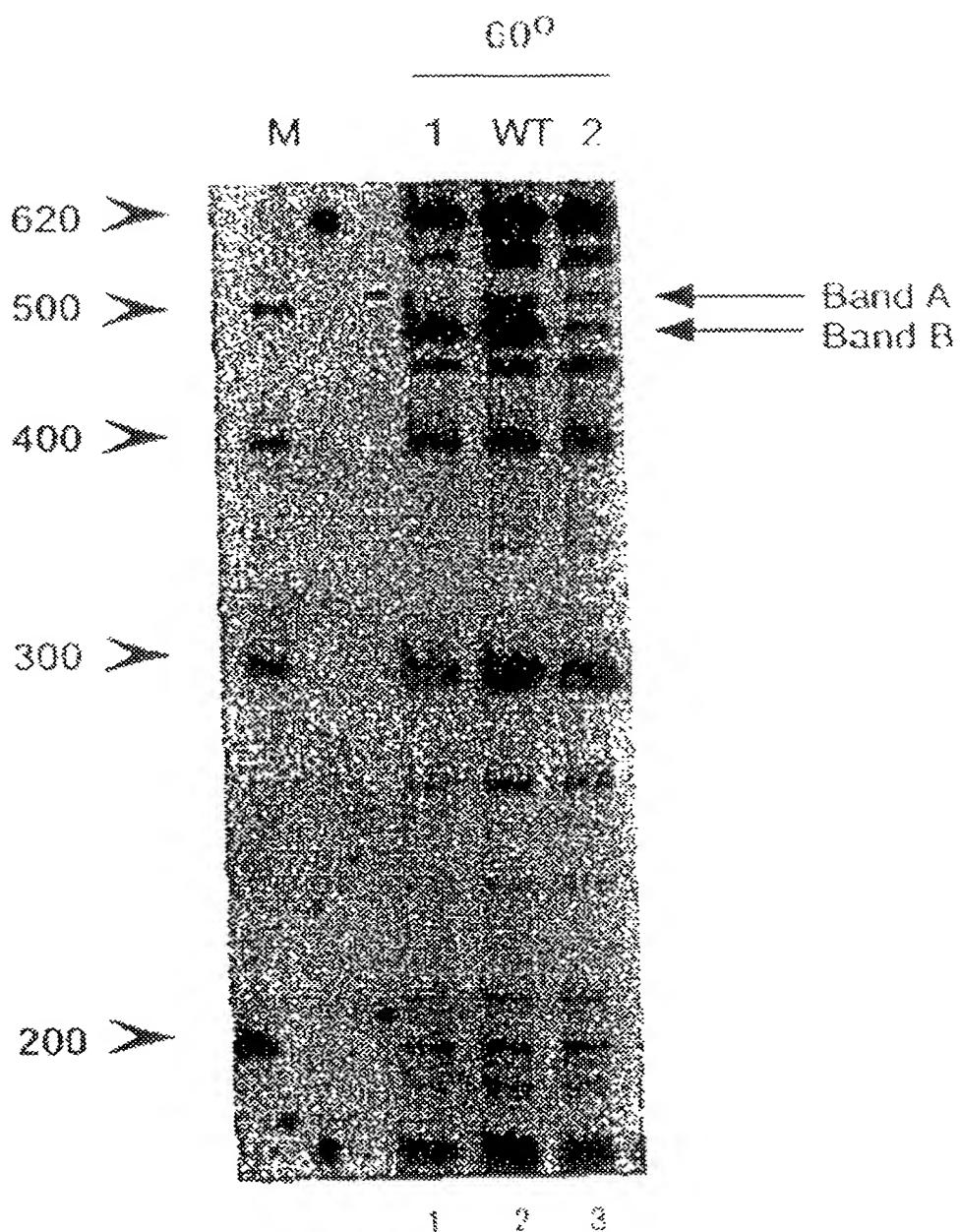
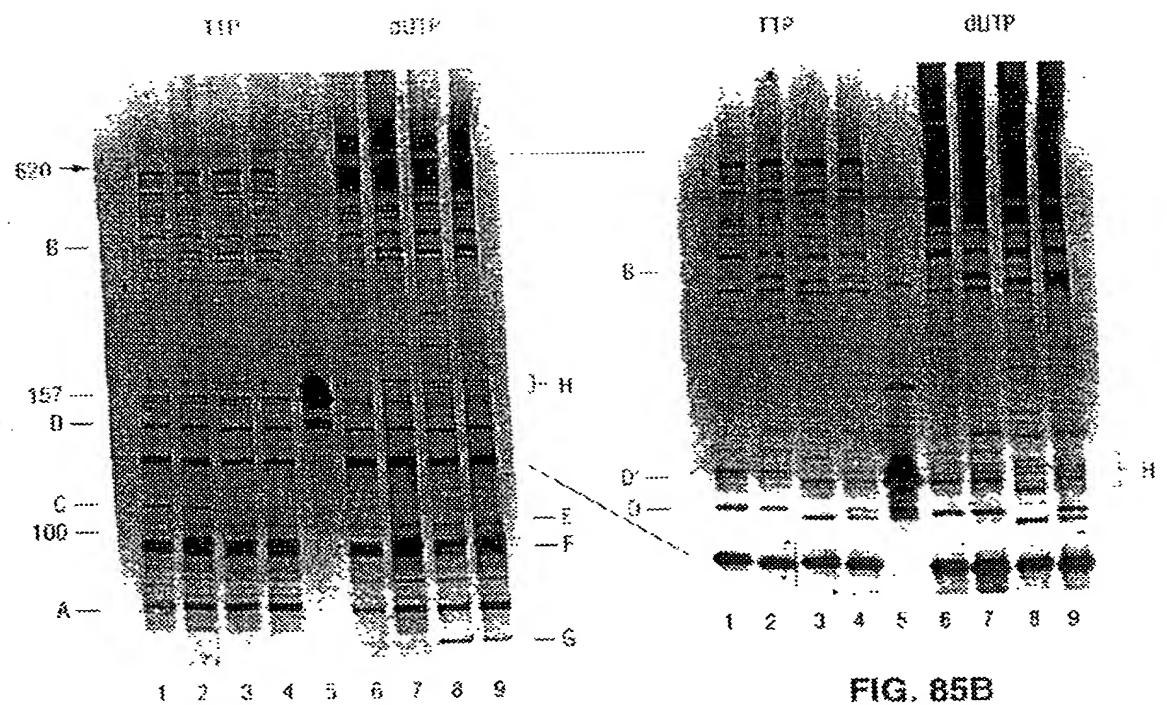


FIG. 84



SENSE STRAND

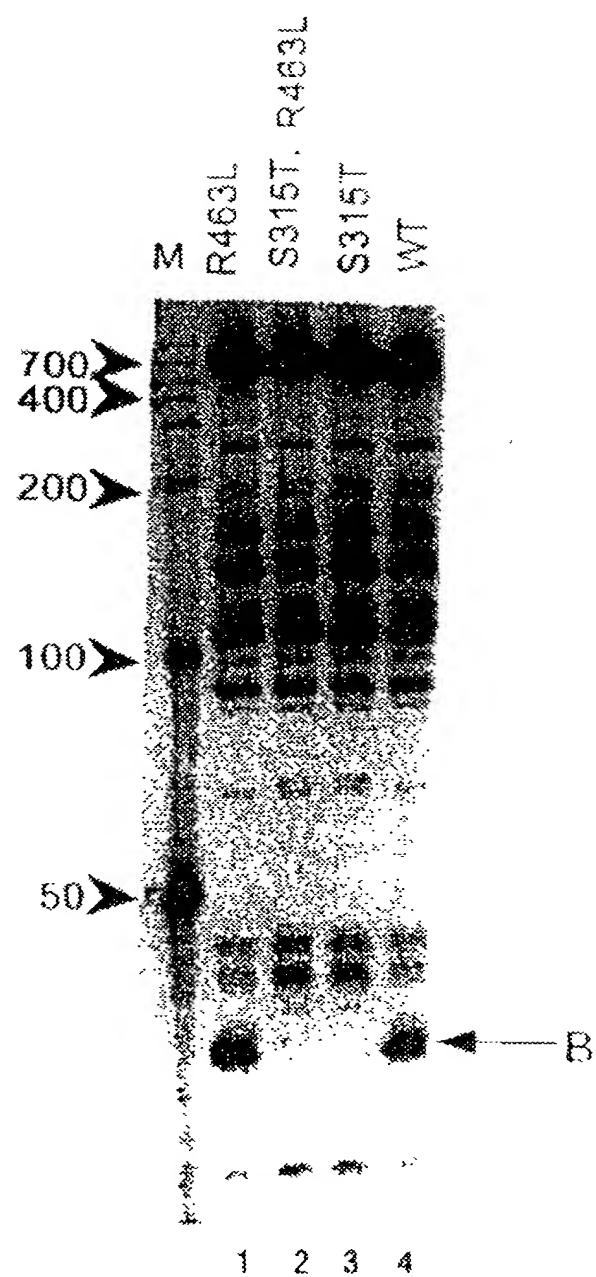


FIG. 86

ANTISENSE STRAND

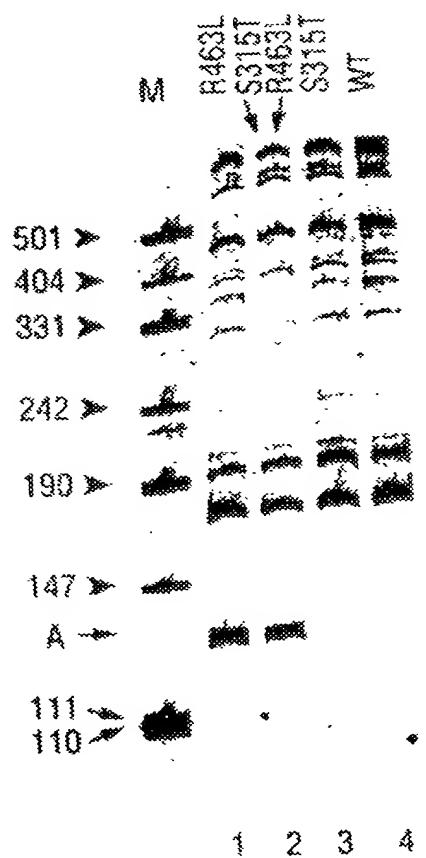


FIG. 87

10	20	30	40	50	60	
AGA	GGCTCAG					
<u>AAATTGAAAGA</u>	<u>GGTTGATCAT</u>	<u>GGCTCAGATT</u>	<u>GAACGCTGGC</u>	<u>GGCAGGCCAA</u>		
TTTAACCTCT	CAAACTAGTA	CCGAGTCTAA	CTTGCACCG	CGTCCCCGAT	TGTGTACGTT	
70	80	90	100	110	120	
						ER10
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACC	AGT <u>GGGGAC</u>	GGGTGAGTAA	
CAGCTGGCA	TTGTCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCTG	GGGTGAGTAA	
130	140	150	160	170	180	
TGTCTGGAA	ACTGCCGTGAT	GGAGGGGGAT	AACTACTGGA	ACGGTAGCT	AATAACGGCAT	
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCAAGATG	
TTGCAGCGTT	CTGGTTCTC	CCCCTGGAAG	CCCCGAAAC	GGTAGCCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGGGG	TAACGGCTCA	CCTAGGGCAC	GATCCCTAGC	TGGTCTGAGA	
CCTAACATGGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGGCTG	CTAGGGATCG	ACCAAGACTCT	
310	320	330	340	350	360	
GGATGACCAAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGGCAGTGG	
CCTACTGGTC	GGTGTACCT	TGACTCTGTG	CCAGGTCTGA	GGATGCCCTC	GTCCGTCAACC	
						1659

**FIG. 88A**

370	380	390	400	410	420
GGAAATTGCG	ACAATGGCG	CAAGCCTGAT	CGAGCCATGC	CGCGTGTATG	AAGAAGGCC
CCTTATAACG	TGTTACCCGC	GTTGGACTA	GTCGGTAGG	GGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TGGGGTTGTA	AAGTACTTTC	AGGGGGAGG	AAGGGAGTAA	AGTTAATAACC	TTTGCTCAT
AGCCCCAACAT	TTCATGAAAG	TGCCCTCTCC	TTCCCTCATT	TCATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGGTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGGCCA	GCAGCCGCC	TAATACGGAG
CTGCCAATGGG	CGTCTCTTC	GTGGCGATT	GAGGCACGGT	CGTCGGGCC	ATTATGCCCTC
550	560	570	580	590	600
GGTCCAAGCG	TTAATGGAA	TTACTGGCG	TAAAGGCCAC	GCAGGGCGTT	TGTTAAGTC
CCACGGTTCGC	AATTAGCCCTT	AATGACCCGC	ATTTCGGTG	CGTCCGCCAA	ACAAATTCACT
610	620	630	640	650	660
GATGTGAAT	CCCCGGGCTC	AACCTGGAA	CTGCATCTGA	TACTGGCAA	CTTGAGTCTC
CTACACTTA	GGGGCCCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCCGTT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCC	TAGAGATCTC	GAGGAATAAC
CATCTCCCC	CATCTTAAGG	TCCACATCGC	CACTTACGC	ATCTCTAGAC	CTCCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGAAGAC	TGACGGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGGCTTC	GGGGGGGGAA	CCTGCTTCTG	ACTGCGAGTC	CACGGCTTTCG	CACCCCTCTG

**FIG. 88B**

SB-4  
CGGGAACTCA AAGGAGACTG CCAGTGTAA ACTGGAGGA GGTGGGATG ACGTCAAGTC  
GCGCTTGACTT TTCCCTGTAC GGTCACTATT TGACCTCCTT TGCAGTTAG

FIG. 88C

					SB-3
					SB-4
1210	1220	1230	1240	1250	1260
ATCATGGCCC	TTA				
ATCATGGCCC	TTACGAA				
<u>ATCATGGCCC</u>	<u>TTACGACCAG</u>	GGCTACACAC	GTGCTACAAT	GGCCATACA	AAGAGAACCG
<u>ATCATGGCCC</u>	<u>TTACGCTGGTC</u>	CCGATGTGT	CACGATGTTA	CCGGTATGT	TTCTCTTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCCGTGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTGGCT	GGAGTATTT	ACGCCAGCATC	AGGCCTAACCC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATAACGT
AGCTGAGGTA	CTTCAGGCCCT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACITTAATGCA</u>
			GC	CACTTATGCA	
1390	1400	1410	1420	1430	1440
TCCCCGGCCT	TGTACACACC	CCCCGTACAA	CATGGGAGT	GGGTTGCCAA	AGAAGTAGGT
<u>AGGGCCCCGA</u>	<u>ACATGTTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA
					1743
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TGTGATTC	TGACTGGGT	GAAGTCGTAA
TCGAATTGGAA	AGCCCTCCCC	CGAATGGTA	AACACTAAGT	ACTGACCCCA	CTTCAGGATT
1510	1520	1530	1540	1550	
CAAGGTAACC	GTAGGGAAC	CTGGGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCCTTG	GACGCCAAC	TAGTGGAGGA	AT.....	

**FIG. 88D**

1638 (SEQ_ID NO:151) E.colirrSE (SEQ_ID NO:158) 0 Cam. jejuns (SEQ_ID NO:159) 0 Stp. aureus (SEQ_ID NO:160) 0	AGAGTTGATCCTGGCTCAG AAATTGAAGAGTTGATCATGGCTCAGATTGAACCGCTGGGGCAGGCCCTAACACATGCA TTTTTATGGAGAGTTGATCCGTGCTCAGGTGAACCGCTGGGGTGCCTAACATGCA TTTTTATGGAGAGTTGATCCGTGCTCAGGTGAACCGCTGGGGTGCCTAACATGCA
	GGCGGACGGG
ER10 (SEQ_ID NO:152) E.colirrSE Cam. jejuns Stp. aureus	60 AGTCGAACGGTAACAG-----GAAGAAGCTTGCCTCTT-----GCTGACGAGTGGCGACGGG 62 AGTCGAACGGAT-----GAAGCTTCTAGCTTAGAAGTGG-----TTAGTGGCGACGGG 61 AGTCGAACGGAA-----GGACGAGAAGCTTGCCTCTGATG-----TTAGCGGGGACGGG
	TGAGTAA
ER10 E.colirrSE Cam. jejuns Stp. aureus	114 TGAGTAATGTCGGGAAACTGCCTGATGGAGGGATAACTACTGGAAACGGTAGCTAATA 114 TGAGTAAGGTATAAGTTAACACAGTGGCTACACAAGAGGACAACAGTGGCTAGAAGTGG-----TTAGTGGCGACGGG 113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGATAACTTCGGGAAACCGGGAGCTAATA
E.colirrSE Cam. jejuns Stp. aureus	175 CCCGATAAC-----GTGGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCCTTTG 176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-----GAAAAG-----TTTTT-----GG 175 CGGGATAATTTTGAAACCGCATGGTCAAAGTGAAGAACGGT-----CTT-----GCTGTCAT
E.colirrSE Cam. jejuns Stp. aureus	221 CCATCGGATGCCAGATGGATTAGCTAGTAGGTGGGTAACCGGCTCACCTAGGGGACGA 221 GTGTAGGGATGAGACTATATAGTATAGCTAGTTGGTAAGGTAAATGGCTTACCAAGGGTATGA 229 CTTATAGATGGATCCGGCTGCATTAGCTGGTAAGGTAAACGGCTTACCAAGGGAACGA
E.colirrSE Cam. jejuns Stp. aureus 1659 (C0MPL)	283 TCCCTAGCTGGCTGAGAGGATGACCACACTGGAACTGAGACACGGTCCAGACTCCTA 283 CGCTTAACTGGCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA 291 TACGTAGCCGACCTGAGAGGGTATGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA ACTCCTA

**FIG. 89A**

E. coli rrSE  
Cam. jejuniS  
Stp. aureus  
1659 (COMPL)

345 CGGAGGGAGCAGTGGGAATATTGCCACAATGGGCCAAGGCCTGATGCCCATGCCCGCTG  
345 CGGAGGGAGCAGTGGGAATATTGCCAATGGGGAAACCCCTGACGCCAACGGCGT  
353 CGGAGGGAGCAGTGGGAATTTCCCAATGGCCAAAGGCCATGCCAACGGCGT  
CGGAGGGAGCAG  
407 TATGAAGAAGGCCTTCGGTTGTAAGTACTTTCAAGGGGGAGGAA-GGGAGGTAAAGTTAAT  
407 GAGGATGACACTTTCGGAGCTAAACTCCCTTAGGAAG AATT  
415 AGTGATGAAGGTCTCGGATCGTAAAACTCTGTTATTAGGAAAGAACATATGTGTAAGTAAC  
468 ACCTTTGCTCATTGACGTTACCCGCAAGAAGAACGGCTAACTCCGTGCCAGCACGCC  
455 C-----TGACGGTACCTAAGGAATAAGCACGGCTAACTCCGTGCCAGCACGCC  
476 TGTGCACATTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCACGCC

**FIG. 89B**

E. coli rrSE	530	GTAATACGGAGGGTCAAGCGTTAATCTGGAAATTACTGGCGTAAAGCCACGCCAGGGGGTTT
Cam. jejuns	506	GTAAATACGGAGGGTCAAGCGTTAATCTGGAAATTACTGGCGTAAAGCCACGCCAGGGGGTT
Stp. aureus	538	GTAAATACGTAGGTGGCAAGCGTTATCCGGAAATTATGGCGTAAAGCCACGCCAGGGGGTT
E. coli rrSE	592	GTTAAAGTCAGATGTTGAATCCCCGGCTCAACCTGGGAACCTGGCATCTGATACTGGCAAGCTT
Cam. jejuns	568	ATCAAAGTCTTGTGAAATCTAACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCT
Stp. aureus	600	TTTAAAGTCTGATGTTGAATGGGGTCATTGGAAACTGGAAACTGGAAACTGGAAACTGGAAACTT
E. coli rrSE	654	GAGTCTCGTAGAGGGGGTAGAATTCCAGGTGTAAGGGTAGAGATCTGGAGGA
Cam. jejuns	630	GAGTGGGGAGAGGCAGATGGAATTGGTGGTGGTGGTAAATCCGTAGATATGGAGGA
Stp. aureus	662	GAGTGCAGAAGAGGAAGTGAATTCCATGTTAGCGGTGAATGGCAGAGATATGGAGGA
E. coli rrSE	716	ATACCCGGTGGCGAAGGGGGCCCTGGACGACTGACGCTCAGGTGCGAAAGCGTGGGGGA
Cam. jejuns	692	ATACCCATTGGGAAGGGGATCTGCTGGAAACTCAACTGACGCTAAGGGGGAAAGCGTGGGGGA
Stp. aureus	724	ACACCCAGTGGCGAAAGGGGACTTCTGGCTGTAACTGACGCTGATGTCGAAAGCGTGGGGGA
E. coli rrSE	778	GCAAACAGGATTAGATAACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGAGGGTTGTGC
Cam. jejuns	754	GCAAACAGGATTAGATAACCCCTGGTAGTCCACGCCCTAAACGATGTCACACTAGTTGGGGGT
Stp. aureus	786	TCAAACAGGATTAGATAACCCCTGGTAGTCCACGCCGTAAACGATGTCATAAGTGTAGGGGG

**FIG. 89C**

<i>E. coli</i> rrSE	840	C- <u>CTTGA</u> -GGCGTGGCTTCCGGAGCTAACGGGTTAACGTCACCCGCCTGGGGAGTACGGCTACGGTGC
<i>Cam. jejuni</i> 5	816	G- <u>CTAGT</u> -CATCTCAGTAATGCAGCTAACGCCATTAAAGTGTACCCGCCTGGGAGTACGGTACGGTGC
<i>Stp. aureus</i>	848	GT- <u>TTCCGGCCCTTAGT</u> GCTGCAGCTAACGCCATTAAAGCACTCCGCCTGGGAGTACGGACCGC
<i>E. coli</i> rrSE	900	AAGGTTAAACTCAAATGAATTGACGGGGCCCCCACAAAGCGGTGGACATGTGGTTAATT
<i>Cam. jejuni</i> 5	876	AAGATTAAACTCAAAGGAATTAGACGGGGACCCGACAAAGCGGTGGACATGTGGTTAATT
<i>Stp. aureus</i>	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGACAAAGCGGTGGACATGTGGTTAATT
<i>E. coli</i> rrSE	962	CGATGCAACGGCAAGAACCTTACCTGGTCTTGACATCACCGGAAGGTTCAAGAGATGAGAAT
<i>Cam. jejuni</i> 5	938	CGAAGATAACGGAAAGAACCTTACCTGGGCTTGATATCTAAGAACCTTAAAGATAAGAGG
<i>Stp. aureus</i>	971	CGAAGCAACGGAAAGAACCTTACCAAATCTGACATCTTGAACAATTAGAGATAGAGCC
<i>E. coli</i> rrSE	1024	GT <u>G-2-CCTTCGGG-2-AA-CCGTGAGACAGGTGCTGCATGGCTCGTCA</u> GCTCGTGTGTTGTA
<i>Cam. jejuni</i> 5	1000	GTGCTAGCTTGTCTAGAA- <u>CTTAGAGACAGGTGCTGCAGCTCGTGTGTTGTA</u>
<i>Stp. aureus</i>	1033	TT <u>CC-2-CCTTCGGG-2-GGACAAAGT</u> GACAGGTGTTGTCATGGCTCGTGTGTTGTA
SB-1		GCAACGGAGGCCAACCC
<i>E. coli</i> rrSE	1081	AATGTTGGGTTAACGTCCTTGTGCTTCCTTATCCTTGTGCTAACGGTTGG- <u>CC</u>
<i>Cam. jejuni</i> 5	1061	GATGTTGGGTTAACGAGGCCAACGGCAACCCACGTATTAGTTAGCTTAAAGCTTAAAGCTAACCC
<i>Stp. aureus</i>	1092	GATGTTGGGTTAACGAGGCCAACGGCAACCCCTTAAGCTTAAAGCTTAAAGCTAACCC

**FIG. 89D**

SB-3 (SEQ ID NO: 157)  
SB-4 (SEQ ID NO: 154)

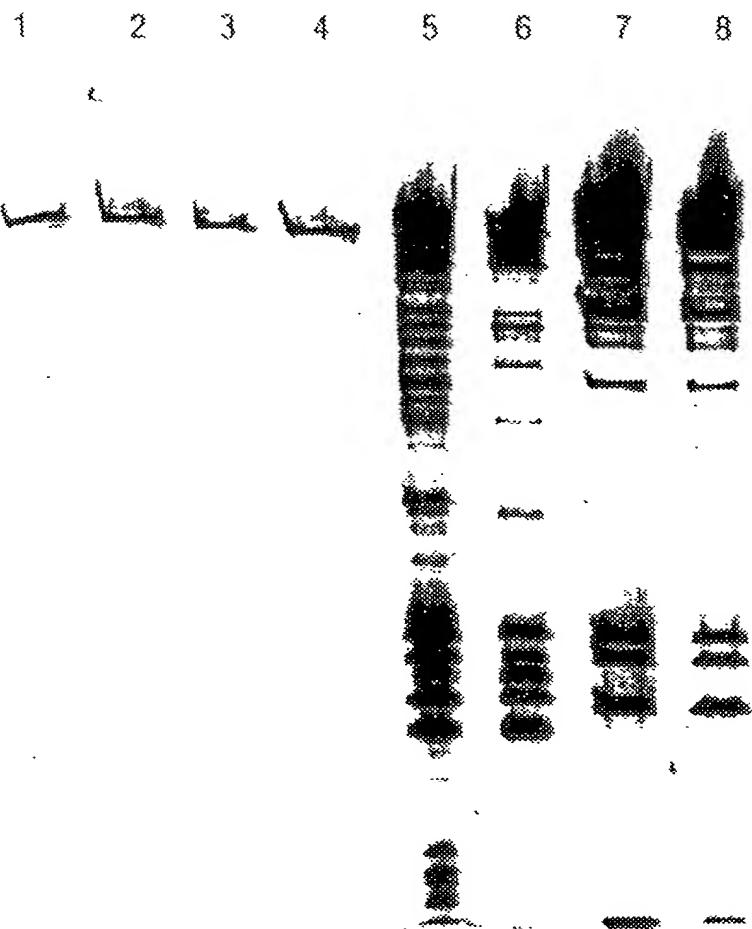
ATGACGTCAAGTCATC  
ATGACGTCAAGTCATC  
CATGACGTCAAGTCATC

SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E. coli rrSE	1204	ATGGCCCTTACGACCAGGGCTACACACCGTGCATAAATGGGCATAAAGAGAACCTC
Cam. jejuns	1183	ATGGCCCTTATGCCAGGGACACACCGTGCATAAATGGCATATAAGAATGGACCAATTACCAAGGAAACC
Stp. aureus	1214	ATGGCCCTTACACACGTGCTACAATGGACAAATACAAGGGAGCCAA
E. coli rrSE	1266	GCGAGAGCAAGGGCACCTCATAAAGTGGCTGTAGTCCGGATTGGAGTCTGCAACTCGACT
Cam. jejuns	1245	GCGAGGGTGGAG-CAAATCTATAAAATATGTCGAACTCGAGAG
Stp. aureus	1276	GCGAGGGTCAAGGAAATCCCATAAAAGTTGTTCTCAGTTGGATTGTA
E. coli rrSE	1328	CATGAAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACTGGTCCCCGGC
Cam. jejuns	1306	CATGAAAGCCGGAAATCGCTAGTAATCGTAGATCAGGCTACGGTACGGTGAATACTGGTCCCCGGG
Stp. aureus	1338	CATGAAAGCTGGAAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTACGGTGAATACTGGTCCCCGGG
	1743 (compl)	CGGTGAATACTGGTCCCCGGG

**FIG. 89E**

**FIG. 89F**

E. coli rrSE	1389	CTTGTACACACCCGCCGTACACCATTGGAGTTGCAAAAGAAGTAGGTAGCTTAACCT
Cam. jejun5	1368	CTTGTACTCACCGCCCGTCACACCATTGGAGTTGATTTCACTCGAACGCCGAATACT <u>-A-A</u>
Stp. aureus	1399	ATTGTACACACCCGCCGTACACCAGGAGTTGTAACACCCGAAGCCGTAACAGGTAAACCT
		CTTGTAC
E. coli rrSE	1451	TCG <u>-G</u> GAGGGCCGCTTACCACTTTGTGATTCATGACTGGGTGAAGTCGTAACAAGGTAAACCG
Cam. jejun5	1427	AC <u>--T</u> AGTTACCGTCCACAGTGGAAATCAGCGACTGGGTGAAGTCGTAACAAGGTAAACCG
Stp. aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGACAAATGATTGGGTGAAGTCGTAACAAGGTAGCCG
E. coli rrSE	1512	TAGGGGAACCTGGGGTGGATCACCTCCCTA---
Cam. jejun5	1485	TAGGAGAACCTGGGGTGGATCACCTCCCT---
Stp. aureus	1523	TATCGGAAGGTGGCTGGATCACCTCCCTTTCT-



**FIG. 90**

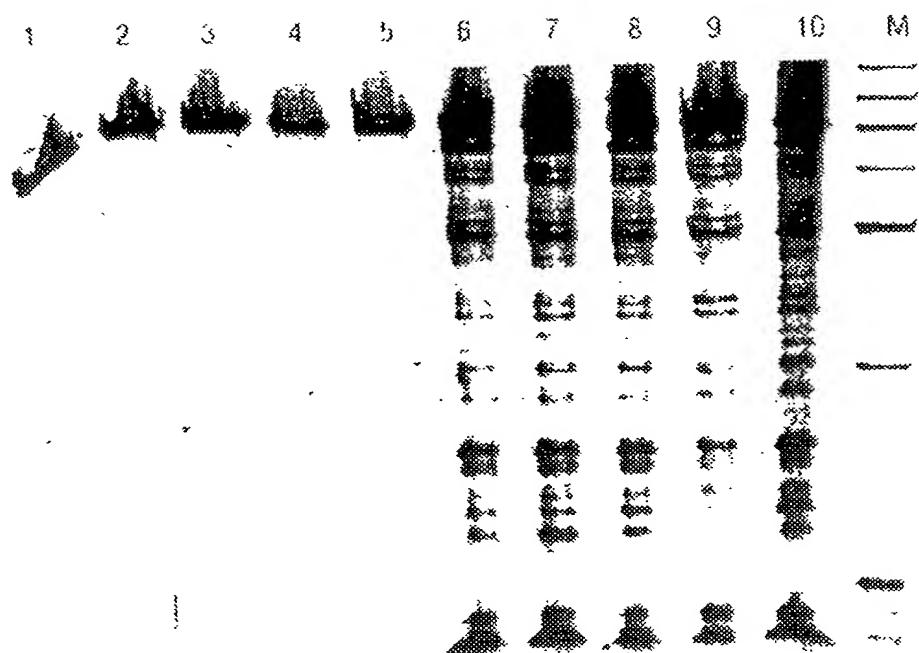


FIG. 91A

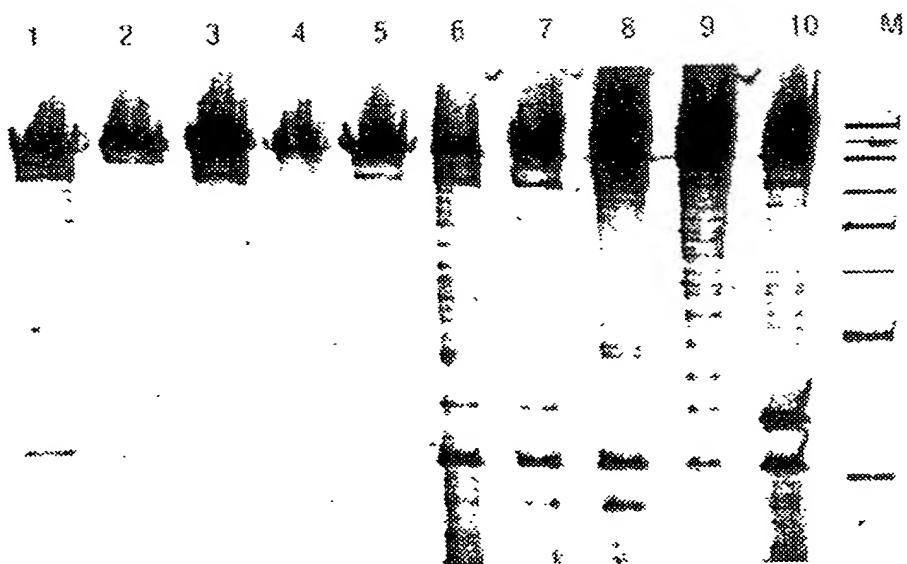


FIG. 91B

1 2 3



FIG. 92

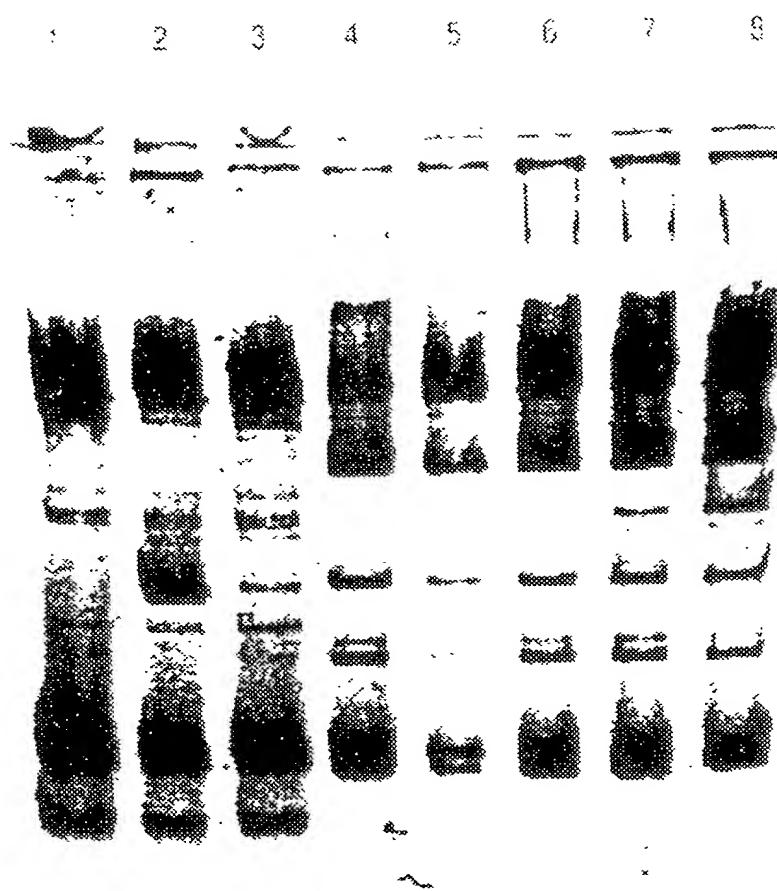


FIG. 93

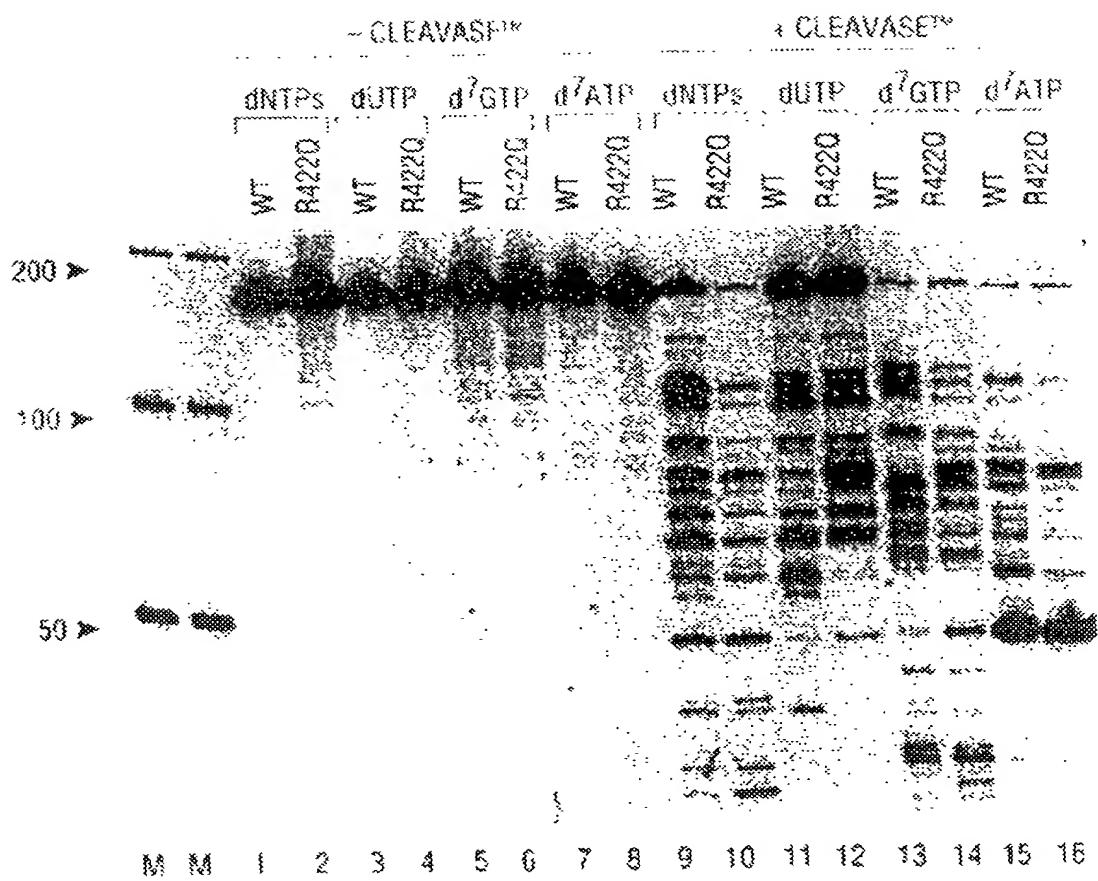


FIG. 94